

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 18:05:26 ; Search time 1878 Seconds
(without alignments)
5363.528 Million cell updates/sec

Title: US-10-089-473a-2

Perfect score: 213

Sequence: 1 ggaagaagatgctgctg.....ccagaatcccttcacgtcc 213

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_lm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_yi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	213	100.0	222	5	AY005480 Gloydius
2	209.8	98.5	1989	5	AF051789 Gloydius
3	206.6	97.0	234	5	AY259516 Bothrops
4	201.8	94.7	712	5	AY204249 Gloydius
5	201.8	94.7	1977	5	AY204245 Gloydius
6	201.8	94.7	2045	5	AF345931 Bothrops
7	198.6	93.2	270	5	AY551929 Gloydius
8	198.6	93.2	318	5	AF054626 Gloydius
9	198.6	93.2	972	5	AF367868 Gloydius
10	198.6	93.2	1558	6	AGKARA D88870 Rgkistron
11	198.6	93.2	1558	6	EO5552 CDNA encodi
12	197	92.5	222	6	AK005242 Sequence
13	197	92.5	917	5	AF367867 Gloydius
14	197	92.5	2027	5	AF051788 Gloydius
15	195.4	91.7	1983	5	AB059572 Trimeres
16	193.8	91.0	222	6	E39840 Anticancer
17	193.8	91.0	222	6	AR287876 Sequence
18	193.8	91.0	2017	5	TCRTRCRA X51530 Trimeresu
19	190.6	89.5	2018	5	AF212305 Agkistrod

20	190.6	89.5	2029	6	BD244771 Confortro
21	190.6	89.5	2029	6	AR489412 Sequence
22	190.6	89.5	2031	5	AB078804 Agkistrod
23	189	88.7	2029	5	AB078806 Agkistrod
24	185.8	87.2	2102	6	AX928621 Sequence
25	184.2	86.5	1205	5	AY258153 Bothrops
26	182.6	85.7	712	5	AY204248 Gloydius
27	182.6	85.7	1992	5	AY204244 Gloydius
28	179.4	84.2	1929	5	AF051790 Gloydius
29	177.8	83.5	1475	5	TXMETRIS X77089 T. mucrosqua
30	176.2	82.7	222	5	AF5197762 PROCOBCH
31	176.2	82.7	1482	5	AF011909 Trimeresu
32	176.2	82.7	2028	5	AB059571 Trimeresu
33	174.8	82.1	2009	5	AB059571 Trimeresu
34	173.2	81.3	1455	5	AY644231 Trimeresu
35	173	81.2	540	5	AF055337 Gloydius
36	173	81.2	1999	5	AY037808 Trimeresu
37	171.4	80.5	213	5	AF0133345 Agkistrod
38	171.4	80.5	1471	5	AF162086 Delnagkis
39	171.4	80.5	1476	5	AAJ3283 Agkistrod
40	171.4	80.5	1863	5	AF117636 Delnagkis
41	171.4	80.5	1863	5	AF117637 Delnagkis
42	168.2	79.0	1446	5	AY67902 Trimeresu
43	167	78.4	911	6	AR043807 Sequence
44	166.8	78.3	1467	5	AY071905 Gloydius
45	166	77.9	2001	5	AB052155 Trimeresu

ALIGNMENTS

RESULT 1
LOCUS AY005480 222 bp mRNA linear VRT 23-AUG-2000
DEFINITION Gloydius halys saxatilis mRNA, partial cds.
ACCESSION AY005480
VERSION AY005480.1 GI:9945027
KEYWORDS
SOURCE Gloydius halys (halys viper)
ORGANISM Gloydius halys

REFERENCE
1 (bases 1 to 222)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.

AUTHORS Chung, K.-H., Koh, Y.-S., Hong, S.-Y. and Kim, D.-S.

TITLE Unpublished Snake venom disintegrin, saxatilis CDNA

REFERENCE 2 (bases 1 to 222)
Chung, K.-H., Koh, Y.-S., Hong, S.-Y. and Kim, D.-S.

AUTHORS Direct Submission

JOURNAL Submitted (24-JUL-2000) Biochemistry, Yonsei Univ., Seodaemun Ku
Shincheon Dong 134, Seoul 120-749, Korea

FEATURES
source location/Qualifiers
1..222

/organism="Gloydius halys"
/mol_type="mRNA"
/db_xref="taxon:8714"
/feature_type="venom gland"
CDS
1..222
/note="disintegrin"
/codon_start=1
/product="saxatilis"
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TTCMRAGDDMDVYCNGISAGCFRPFPA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4,3e-57;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
GY 1 GGAGAGATGTGACTGTGGCGCTCTGCAATCCGTGTGCGAGATGCTGCAACTGTGTA 60

Db 7 GGAGAGAAATGATGCTGCGCTCTCTGCAAAATCCGTCGATGCTGCAACTGTAA 66
Qy 61 CTGAGACACAGGGGCGGCGAGTGTGCAAGAGAGCTGTGTGACCGTGCAGATTATGAAA 120
Db 67 CTGAGACACAGGGGCGGCGAGTGTGCAAGAGAGCTGTGTGACCGTGCAGATTATGAAA 126
Qy 121 GAAGGAACATATATGCGGATGCAAGAGGGGTATGATGATGATTAATGCAATGCGATA 180
Db 127 GAAGGAACATATATGCGGATGCAAGAGGGGTATGATGATGATTAATGCAATGCGATA 186
Qy 181 TCTGCTGCTGTCTCCAGAAATCCCTTCATGCC 213
Db 187 TCTGCTGCTGTCTCCAGAAATCCCTTCATGCC 219

RESULT 2
AF051789 1989 bp mRNA linear VRT 08-NOV-1999
LOCUS Gloydius halys metalloprotease (Mt-d) mRNA, complete cds.
DEFINITION AF051789
ACCESSION AF051789.1 GI:4106004
VERSION
KEYWORDS
SOURCE Gloydius halys (hals viper)
ORGANISM Gloydius halys
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
REFERENCE
AUTHORS Jeon, O.H. and Kim, D.S.
TITLE Molecular cloning and functional characterization of a snake venom metalloprotease
JOURNAL Eur. J. Biochem. 263 (2), 526-533 (1999)
MEDLINE 99337693
PUBMED 10406963
REFERENCE 2 (bases 1 to 1989)
AUTHORS Jeon, O.H. and Kim, D.S.
TITLE Direct Submission
JOURNAL Submitted (03-MAR-1998) Biochemistry, Yonsei University, 134
Shincheon-dong Seodaemun-Gu, Seoul 120-749, Korea

FEATURES
source
1..1989
/organism="Gloydius halys"
/mol_type="mRNA"
/strain="brevicaudus"
/db_xref="taxon:8714"
/tissue_type="venom"
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/gene="Mt-d"
51..1499
/gene="Mt-d"
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/product="metalloprotease"
/protein_id="AA02654.1"
/db_xref="GI:4106005"
/translation="MTQVLTITCLAAFPYQGGSMILESGNVDYEVVYQKYPALPK
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DEAPKCVCTQTNKSDPILKASQVLTAEQRPORYELVVVAADGKTKYDSND
TITVMEHLVANNINEFYSILNVRYSLTLELMSMODLINVQSAADLTLEAFGRND
LNRISNDHNOCHCCGANSVMDYLRVGSYFSPDCKNEVQTYTTPDNPCITANE
LGNLGNHDNOCCHCCGANSVMDYLRVGSYFSPDCKNEVQTYTTPDNPCITANE
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ORIGIN
Query Match 98.5%; Score 209.8; DB 5; Length 1989;
Best Local Similarity 99.1%; Pred. No. 4.5e-56;
Matches 211; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGAGAAAGATGATGCTGCGCTCTCTGCAAAATCCGTCGATGCTGCAACTGTAA 60
Db 1284 GGAGTTGAATGATGCTGCGCTCTCTGCAAAATCCGTCGATGCTGCAACTGTAA 1343

Qy 61 CTGAGACACAGGGGCGGCGAGTGTGCAAGAGAGCTGTGTGACCGTGCAGATTATGAAA 120
Db 1344 CTGAGACACAGGGGCGGCGAGTGTGCAAGAGAGCTGTGTGACCGTGCAGATTATGAAA 1403
Qy 121 GAAGGAACATATATGCGGATGCAAGAGGGGTATGATGATGATTAATGCAATGCGATA 180
Db 1404 GAAGGAACATATATGCGGATGCAAGAGGGGTATGATGATGATTAATGCAATGCGATA 1463
Qy 181 TCTGCTGCTGTCTCCAGAAATCCCTTCATGCC 213
Db 1464 TCTGCTGCTGTCTCCAGAAATCCCTTCATGCC 1496

RESULT 3
AY259516 234 bp mRNA linear VRT 03-APR-2003
LOCUS Bothrops alternatus disintegrin mRNA, partial cds.
DEFINITION AY259516
ACCESSION AY259516.1 GI:29501767
VERSION
KEYWORDS
SOURCE Bothrops alternatus
ORGANISM Bothrops alternatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
REFERENCE
AUTHORS Ramos, O.H.P. and Seliestre-de-Araujo, H.S.
TITLE Cloning and expression of disintegrins from Bothrops alternatus
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 234)
TITLE Direct Submission
JOURNAL Submitted (20-MAR-2003) Depto. de Ciencias Fisiologicas,
Universidade Federal de Sao Carlos, Rodovia Washington Luis
(SP-310), Km 235, Sao Carlos, Sao Paulo 13565-905, Brazil

FEATURES
source
1..234
/organism="Bothrops alternatus"
/mol_type="mRNA"
/db_xref="taxon:64174"
1..234
/note="Disba-01; belongs to the RGD family of
disintegrins"
/codon_start=1
/product="disintegrin"
/protein_id="AA075107.1"
/db_xref="GI:29501768"
/translation="NELLEAGSECDGTPNPPCDATCKLRPGAQCAEGLCCDQCRP
MKEGTICRMARDMDYDNGISAGCPNPFHA"

ORIGIN
Query Match 97.0%; Score 206.6; DB 5; Length 234;
Best Local Similarity 98.1%; Pred. No. 4.8e-55;
Matches 209; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGAAAGATGATGCTGCGCTCTCTGCAAAATCCGTCGATGCTGCAACTGTAA 60
Db 19 GGAGAAAGATGATGCTGCGCTCTCTGCAAAATCCGTCGATGCTGCAACTGTAA 78
Qy 61 CTGAGACACAGGGGCGGCGAGTGTGCAAGAGAGCTGTGTGACCGTGCAGATTATGAAA 120
Db 79 CTGAGACACAGGGGCGGCGAGTGTGCAAGAGAGCTGTGTGACCGTGCAGATTATGAAA 138
Qy 121 GAAGGAACATATATGCGGATGCAAGAGGGGTATGATGATGATTAATGCAATGCGATA 180
Db 139 GAAGGAACATATATGCGGATGCAAGAGGGGTATGATGATGATTAATGCAATGCGATA 198
Qy 181 TCTGCTGCTGTCTCCAGAAATCCCTTCATGCC 213
Db 199 TCTGCTGCTGTCTCCAGAAATCCCTTCATGCC 231

LOCUS	AY204249	712 bp	mRNA	linear	VRT 01-JUN-2003
DEFINITION	Gloydus ussuriensis disintegrin mRNA, partial cds.				
ACCESSION	AY204249				
VERSION	AY204249.1	GI:31322310			
KEYWORDS					
SOURCE	Gloydus ussuriensis				
ORGANISM	Gloydus ussuriensis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidodonta; Squamata; ScleroGLOSSa; Serpentes; Colubridae; Viperidae; Crotalinae; Gloydus. 1 (bases 1 to 712) Sun, D.-J. and Yang, T.-S. Direct Submission Submitted (17-DEC-2002) Biochemistry Lab, Frontier Medical Science Institute, Jilin University, No. 13 Ximin Street, Changchun, Jilin 130021, China				
FEATURES	Location/Qualifiers				
source	1..712				
	/organism="Gloydus ussuriensis"				
	/mol_type="mRNA"				
	/db_xref="taxon:35671"				
	/tissue_type="snake venom gland"				
	/country="China; northeast area"				
	<1..222				
	/codon_start=1				
	/product="disintegrin"				
	/protein_id="AAP20644.1"				
	/db_xref="GI:31322311"				
	/translation="EAGEBCDSDSPGPPCCDAATCKLPFGAQCABGLCCBGRFMEKGG TVCRIARDMDYDCNGISACFPNPFHA"				
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Query Match	94.7%; Score 201.8; DB 5; Length 712;				
Best Local Similarity	96.7%; Pred. No. 1,7e-53;				
Matches 206;	Conservative	0;	Mismatches	7;	Indels 0; Gaps 0;
QY	1	GGAGAGATGTGACTGTGGGCTTCCTGCAAAATCGTCTCGATGCTGCACCTGTAA	60		
DB	7	GGAGAAGATGTGACTGTGGGCTTCCTGCAAAATCGTCTCGATGCTGCACCTGTAA	66		
QY	61	CTGAGACCGAGGGCGGCACTGTGCGAAGAGATGTGTTGTGACCCAGTGAATTATGAA	120		
DB	67	CTGAGACCGAGGGCGGCACTGTGCGAAGAGATGTGTTGTGACCGTGAATTATGAA	126		
QY	121	GAAAGAACAAATATGCCGATGGCAAGGGGTATGATGATGATTACTGCAATGGCATA	180		
DB	127	GAAAGAACAAATATGCCGATGGCAAGGGGTATGATGATGATTACTGCAATGGCATA	186		
QY	181	TCTGCTGGCTGTCCGAAATCCTTCATGCC	213		
DB	187	TCTGCTGGCTGTCCGAAATCCTTCATGCC	219		
RESULT 5					
LOCUS	AY204245	1977 bp	mRNA	linear	VRT 01-JUN-2003
DEFINITION	Gloydus ussuriensis metalloproteinase/disintegrin ussuriin				
ACCESSION	AY204245				
VERSION	AY204245.1	GI:31322302			
KEYWORDS					
SOURCE	Gloydus ussuriensis				
ORGANISM	Gloydus ussuriensis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidodonta; Squamata; ScleroGLOSSa; Serpentes; Colubridae; Viperidae; Crotalinae; Gloydus. 1 (bases 1 to 1977) Sun, D.-J. and Yang, T.-S. Direct Submission Submitted (17-DEC-2002) Biochemistry Lab, Frontier Medical Science Institute, Jilin University, No. 13 Ximin Street, Changchun,				

Jilin 130021, China
 Location/Qualifiers
 1. 1977
 /organism="Gloydus ussuriensis"
 /mol_type="mRNA"
 /db_xref="taxon:35671"
 /tissue_type="snake venom gland"
 /country="China: northeast area"
 51. 1487
 /codon_start=1
 /product="metalloproteinase/disintegrin ussurin precursor"
 /protein_id="AAP0640.1"
 /db_xref="GI:3122303"
 /translation="MIOVLIVTICLAAPYQGSIIIPSGSNVDYIVPRKVALPK
 GAVPRKEDTMOYELKNGEPVVLHLEKNGLFSGKDYSETHYSPDGKITTNPVEDH
 GAYGRONDADSTASISACNGKHGKHEKQGENVLLPELTSLSBAAPVKEHKEE
 DEPRKMGVTEINWSETEPRKASPLVYTTQRYVELVYVADPRMTKXNGNLIIST
 WVEIEFTINIEITQRMNTHVALVGLFIWSGDKITVQSSADVLDLFGTNGEIDLNR
 KSHDNAGLPTDFDPTIGLAVYGTMCDEKRSYGVQDPSINLLVAVTMAEIGHN
 LGMHNDENYSCCGFACIKSPISPOPSKFSYCSYIHWYTYINRNPCCILKPLRT
 DIVSTPYSGNELLEAGEBCDDSPGNDCCPAATCKLRPAQCAEAGCCEQCRPMKEGT
 VCNLRADDDMDYDCNGISACPRNPFA"
 ORIGIN
 Query Match 94.7%; Score 201.8; DB 5; Length 1977;
 Best Local Similarity 96.7%; Pred. No. 1.6e-53;
 Matches 206; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 Oy 1 GGAAABAATGTGCTGTGGCGCTCCGCAATCCGTCGCGCATGTGCAACCTGTAA 60
 Db 1272 GGAGAAATAATGTGCTGTGACTCTCCGGAATCCGTGCGCATGTGCAACTGTAA 1331
 Oy 61 CTGAGACCAAGGGGCGAGTGTGCAAGAGACTGTGTGTGACCAAGTGCAGATTATGAA 120
 Db 1332 CTGAGACCAAGGGGCGAGTGTGCAAGAGACTGTGTGTGACAGTGCAGATTATGAA 1391
 Oy 121 GAAGGAACAATATGCCGATGGCAAGGGGAGTAGACATGATGATTCTGCAATGGCATA 180
 Db 1392 GAAGGAACAATATGCCGATGGCAAGGGGAGTAGACATGATGATTCTGCAATGGCATA 1451
 Oy 181 TCTGCTGGCTGTCCAGAAATCCCTTCATGCC 213
 Db 1452 TCTGCTGGCTGTCCAGAAATCCCTTCATGCC 1484
 RESULT 6
 AF345931 2045 bp mRNA linear VRT 04-MAR-2001
 LOCUS Bothrops jararaca bothrostratin precursor, mRNA, complete cds.
 ACCESSION AF345931 GI:13194759
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Bothrops jararaca (Jararaca)
 Bothrops jararaca
 Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidodactylia; Squamata; Scleroglossae; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Bothrops.
 REFERENCE
 1 (bases 1 to 2045)
 Silva,C.A., Martins de Camargo,A.C. and de Toledo Serrano,S.M.
 Molecular cloning of a cDNA encoding bothrostratin, a precursor of a
 RGD containing disintegrin from Bothrops jararaca venom
 Unpublished
 2 (bases 1 to 2045)
 Silva,C.A., Martins de Camargo,A.C. and de Toledo Serrano,S.M.
 Direct Submission
 Submitted (05-FEB-2001) Biochimica e Biofisica, Instituto Butantan,
 Av. Vital Brasil 1500, Sao Paulo 05503-900, Brazil
 Location/Qualifiers
 1. 2045
 /organism="Bothrops jararaca"
 /mol_type="mRNA"
 /db_xref="taxon:8724"
 /note="isolated from venom"
 FEATURES
 source

QY 1 GGAGAGAATGCTGCTGGGCTCTCTGCAATCCGCTGCGATGCTGCAACCTGTAA 60
DB 103 GGAGAGAATGCTGCTGGGCTCTCTGCAATCCGCTGCGATGCTGCAACCTGTAA 162
QY 61 CTGAGACCAAGGGGCGGCACTGTGTCAGAGAGACTGTGTTGTGACCAAGTCAATTATGAA 120
DB 163 CTGAGACCAAGGAGCACTGTGTCAGAGAGAGACTGTGTTGTGACCAAGTCAATTATGAA 222
QY 121 GAAGAACATATATGCGGATGCGAAGGGGTGATGACATGATGATTACTGCAATGGCATA 180
DB 223 GAAGAACATATATGCGGATGCGAAGGGGTGATGACATGATGATTACTGCAATGGCATA 282
QY 181 TCTGCTGCTGCTGCCAGAAATCCCTTCATGCC 213
DB 283 TCTGCTGCTGCTGCCAGAAATCCCTTCATGCC 315

RESULT 9
AF367868 972 bp mRNA linear VRT 17-JUL-2001
LOCUS Gloydius halys brevicaudus metalloproteinase (hxl-1) mRNA, partial
DEFINITION cds.
ACCESSION AF367868
VERSION AF367868.1 GI:14794942
KEYWORDS
SOURCE Gloydius blomhoffi brevicaudus
ORGANISM Gloydius blomhoffi brevicaudus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
REFERENCE 1 (bases 1 to 972)
AUTHORS Kilian, H.
TITLE Direct Submission
JOURNAL Submitted (02-APR-2001) Biochemistry, Guangxi Medical University, 6
Shuangyong Road, Nanning, Guangxi 530021, China
LOCATION/Qualifiers
FEATURES
source 1..972
/organism="Gloydius blomhoffi brevicaudus"
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/sub_species="brevicaudus"
/db_xref="taxon:259325"
/tissue_type="venom gland"
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/note="disintegrin"
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/product="metalloproteinase"
/protein_id="AAK73517.1"
/db_xref="GI:14794942"
/translat="EAPMGVLTQWMSYERIKKASQSNLTPAHQRYIELVYADHGM
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ORIGIN
Query Match 93.2%; Score 198.6; DB 5; Length 972;
Best Local Similarity 95.8%; Pred. No. 1.9e-52;
Matches 204; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

DB 859 GAAGAACATATATGCGGATGCGAAGGGGTGATGACATGATGATTACTGCAATGGCATA 918
QY 181 TCTGCTGCTGCTGCCAGAAATCCCTTCATGCC 213
DB 919 TCTGCTGCTGCTGCCAGAAATCCCTTCATGCC 951

RESULT 10
AGKHA 1558 bp mRNA linear VRT 01-FEB-2003
LOCUS Agkistrodon halys mRNA for prepro-halystatin, complete cds.
DEFINITION D28870
ACCESSION D28870
VERSION D28870.1 GI:469189
KEYWORDS
SOURCE Gloydius halys (hals viper)
ORGANISM Gloydius halys
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
REFERENCE 1 (bases 1 to 1558)
AUTHORS Fujisawa, Y., Kuroda, S., Noco, K., Konishi, H. and Terashita, Z.
TITLE Halystatin, a novel disintegrin from agkistrodon halys, is a potent
inhibitor of bone resorption and platelet aggregation
J. Takeda Res. Lab. 53, 39-56 (1994)
REFERENCE 2 (bases 1 to 1558)
AUTHORS Kuroda, S.
TITLE Direct Submission
JOURNAL Submitted (08-MAR-1994) Shun-ichi Kuroda, Osaka University,
Institute of Scientific and Industrial Research, Department of
Structural Molecular Biology; 8-1 Mihogaoka, Ibaraki, Osaka
567-0047, Japan (E-mail: skuroda@sanken.osaka-u.ac.jp,
Tel:81-6-6879-8462, Fax:81-6-6879-8464)
LOCATION/Qualifiers
FEATURES
source 1..1558
/organism="Gloydius halys"
/mol_type="mRNA"
/db_xref="taxon:8714"
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/protein_id="BA06025.1"
/db_xref="GI:469190"
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AAVKVVEDAQYERKVGEPPLHLERKGLFSDYSBHSIPARISAPSVEDH
CEPHRVEDNDASTLSACDGLKAFHFIQGMVLEFLEVDTPAHAVFKYANEKE
DEPFRKCVQWMSYESTKASQQLNPDQRPQRTIKAIYVDHMYKVAENSE
RITKSHOMININMCRALNIVTSLVLRISSEDLITVNASASSTLRGAMETV
ILNRVSHDRAOIMATITINGAVTIGAPVGGWDPERSVAIVDHNALIFIVATMT
MKNHGMHDEKNCNTCINSKUISRQSPSEFSPCENENETVYTTDSPOCILDPL
RPTVSTVPSGSELLEAGBECDSFGNPPCDPAATCKLRQAGCAEGSLCCDQCFMK
GTVCRIARDMDVDYCNGISAGCPNPFA"

ORIGIN
Query Match 93.2%; Score 198.6; DB 5; Length 1558;
Best Local Similarity 95.8%; Pred. No. 1.7e-52;
Matches 204; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Query Match 92.5%; Score 197; DB 5; Length 917;
Best Local Similarity 95.3%; Pred. No. 5.7e-52;
Matches 203; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 GGAGAGAGATGTGACTGTGGCGCTTCGCAATCCGCTGCGTGGATGCTGCAACCTGTAAA 60
DB 702 GGAGAGAGATGTGACTGTGGCGCTTCGCAATCCGCTGCGTGGATGCTGCAACCTGTAAA 761
QY 61 CTGAGACAGGAGGCGCAGTGTGACAGAGAGACTGTGTGTGACCAAGTGCAGATTATGAAA 120
DB 762 CTGAGACAGGAGGCGCAGTGTGACAGAGAGACTGTGTGTGACCAAGTGCAGATTATGAAA 821
QY 121 GAAGAGACAATATGCCGATGCGAGAGGGGTGATGACATGATGATTAAGTCAATGGCATA 180
DB 822 GAAGAGACAATATGCCGATGCGAGAGGGGTGATGACATGATGATTAAGTCAATGGCATA 881
QY 181 TCTGCTGGCTGTCCCGAAGATCCCTTCATGCC 213
DB 882 TCTGCTGGCTGTCCCGAAGATCCCTTCATGCC 914

RESULT 14
AF051788 2027 bp mRNA linear VRT 05-JAN-1999
LOCUS AF051788
DEFINITION Gloydius halys metalloprotease (Mt-b) mRNA, complete cds.
ACCESSION AF051788
VERSION AF051788.1 GI:4106002
KEYWORDS
SOURCE Gloydius halys (halys viper)
ORGANISM Gloydius halys
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
1 (bases 1 to 2027)
Joon,O.H. and Kim,D.S.
Direct Submission
Submitted (03-MAR-1998) Biochemistry, Yonsei University, 134
Shincheon-Dong Seodaemun-Gu, Seoul 120-749, Korea
LOCATION/Qualifiers
1..2027
/organism="Gloydius halys"
/mol_type="mRNA"
/strain="Brevicaudus"
/db_xref="taxon:8714"
/tissue_type="venom"
1..2027
/gene="Mt-b"
19..1536
/gene="Mt-b"
/codon_start=1
/product="metalloprotease"
/protein_id="AAD02653.1"
/db_xref="GI:4106003"
/translation="MIOVLIVITICLAVPPYQSSIIILSGNVVDYEVYPRKVTALPK
GAVQPKEDAVQYERFVNGEAVLVLEKNGKLFSDYSETHYSPGRIITTPSYEDH
CYHGRINDADSTASISACNGKLGHFRLQGETYLIEPLKLSNBEAHAVKEDVEKE
DEARPGCVTONWESYEPIKEDVEKEDEARPGCVTONWESYEPIKKAQSNLTPAH
QRYELIVADHGMFKYNGSDKIRBVRQWNTVAIDVISYMTIDVALGLQIWSNK
DLINVOAPAHTLDSFGKREBDLHLIHNAMLLAIDFGDTIGLAVGTMSNPK
GSTGVODHSTINFRVATMAHEIGNMLGIHDGSSCGSGYSIMSPVISHPSKXF
SDGYTCOWDEITNOKPQICLRLTDIVSTPVSIGNMLLAGEECDCGSPNPPCA
ATCKLRQAQACBELCDDQCQCFMEGTICRRGRDDIDYICNGISACCPNPPHA"

ORIGIN
Query Match 92.5%; Score 197; DB 5; Length 2027;
Best Local Similarity 95.3%; Pred. No. 5.7e-52;
Matches 203; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 GGAGAGAGATGTGACTGTGGCGCTTCGCAATCCGCTGCGTGGATGCTGCAACCTGTAAA 60
DB 1321 GGAGAGAGATGTGACTGTGGCGCTTCGCAATCCGCTGCGTGGATGCTGCAACCTGTAAA 1380
QY 61 CTGAGACAGGAGGCGCAGTGTGACAGAGAGACTGTGTGTGACCAAGTGCAGATTATGAAA 120

Db 1381 CTGAGACAGGAGGCGCAGTGTGACAGAGAGACTGTGTGTGACCAAGTGCAGATTATGAAA 1440
QY 121 GAAGAGACAATATGCCGATGCGAGAGGGGTGATGACATGATGATTAAGTCAATGGCATA 180
DB 1441 GAAGAGACAATATGCCGATGCGAGAGGGGTGATGACATGATGATTAAGTCAATGGCATA 1500
QY 181 TCTGCTGGCTGTCCCGAAGATCCCTTCATGCC 213
DB 1501 TCTGCTGGCTGTCCCGAAGATCCCTTCATGCC 1533

RESULT 15
AB059572 1983 bp mRNA linear VRT 10-OCT-2001
LOCUS AB059572
DEFINITION Trimeresurus elegans mRNA for elegantin-2a precursor, complete cds.
ACCESSION AB059572
VERSION AB059572.1 GI:15991221
KEYWORDS
SOURCE Trimeresurus elegans
ORGANISM Trimeresurus elegans
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
1
Shimosaka,S.
Trimeresurus elegans mRNA for elegantin-2a precursor, complete cds
JOURNAL Published Only in Database (2001)
2 (bases 1 to 1983)
Murrayama,N. and Shimosaka,S.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (09-APR-2001) Nobuhito Murrayama, Showa University, School
of Pharmaceutical Sciences, 1-5-8 Hatanodai, Shingawa-ku, Tokyo
142-8585, Japan (E-mail: murrayama@pharm.showa-u.ac.jp,
Tel:81-3-3784-8203, Fax:81-3-3784-7550)
LOCATION/Qualifiers
1..1983
/organism="Trimeresurus elegans"
/mol_type="mRNA"
/db_xref="taxon:88086"
/sex="female"
/tissue_type="venom gland"
73..1518
/codon_start=1
/product="elegantin-2a precursor"
/protein_id="BAB69658.1"
/db_xref="GI:15991222"
/translation="MIOVLIVITICLAVPPYQSSIIILSGNVVDYEVYPRKVTALPK
GAVQPKEDAVQYERFVNGEAVLVLEKNGKLFSDYSETHYSPGRIITTPSYEDH
CYHGRINDADSTASISACNGKLGHFRLQGETYLIEPLKLSNBEAHAVKEDVEKE
DEARPGCVTONWESYEPIKKAQSNLTPAH QRYELIVADHGMFKYNGSDKIRBVRQWNTVAIDVISYMTIDVALGLQIWSNK
DLINVOAPAHTLDSFGKREBDLHLIHNAMLLAIDFGDTIGLAVGTMSNPK
GSTGVODHSTINFRVATMAHEIGNMLGIHDGSSCGSGYSIMSPVISHPSKXF
SDGYTCOWDEITNOKPQICLRLTDIVSTPVSIGNMLLAGEECDCGSPNPPCA
ATCKLRQAQACBELCDDQCQCFMEGTICRRGRDDIDYICNGISACCPNPPHA"

ORIGIN
Query Match 91.7%; Score 195.4; DB 5; Length 1983;
Best Local Similarity 94.8%; Pred. No. 1.8e-51;
Matches 202; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGAGAGAGATGTGACTGTGGCGCTTCGCAATCCGCTGCGTGGATGCTGCAACCTGTAAA 60
DB 1303 GGAGAGAGATGTGACTGTGGCGCTTCGCAATCCGCTGCGTGGATGCTGCAACCTGTAAA 1362

QY	61	CTGAGACCAAGGGGCGCACTGTGCAAGAGACTGTGTGTGTGACCAAGTGCAGATTATGAAA	120
Db	1363	CTGAGACCAAGGGGCGCACTGTGCAAGAGACTGTGTGTGTGACCAAGTGCAGATTATGAAA	1422
QY	121	GAAGGACCAATATATGCGGATGCGCAAGGGGTGATGACATGATGATTACTGCAATGGCATA	180
Db	1423	GAAGGATATATATGCGGATGCGCAAGGGGTGATGACATGATGATTACTGCAATGGCATA	1482
QY	181	TCTGCTGGCTGTCCAGAAATCCCTTCATGCC	213
Db	1483	TCTGCTGGCTGTCCAGAAATCCCTTCATGCC	1515

Search completed: December 3, 2004, 19:18:46
 Job time : 1880 secs


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OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Gloydus.
OX NCB1_TaxID=8714;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Fujisawa Y., Kuroda S., Notoya K., Konishi H., Terashta Z.;
RT "Halysantin, a novel disintegrin from agkistrodon halys, is a potent
inhibitor of bone resorption and platelet aggregation.";
RU Takeda Kenyusho Ho 53:39-56 (1994).
DR EMBL; D28871; BAA06027.1; -.
DR MEROPS; M12.134; -.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Peptidase_M12B.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; Disintegrin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MERPO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
FT NON_TER
SQ SEQUENCE 117 AA; 12686 MW; B1F9A98056BAB07B CRC64;

Query Match
Best Local Similarity 99.3%; Score 430; DB 2; Length 117;
Pred. No. 1.1e-35;
Matches 72; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAGEBCDDGAPNPCCDAATCTLRPGACCAEGLCCDQCRFMKEGTCRMARGDDMDYCN 60
DB 45 EAGEBCDDGAPNPCCDAATCTLRPGACCAEGLCCDQCRFMKEGTCRMARGDDMDYCN 104
QY 61 GISACCPNPFHA 73
DB 105 GISACCPNPFHA 117

RESULT 3
Q9PVK9 PRELIMINARY; PRT; 482 AA.
AC Q9PVK9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Metalloprotease.
GN Name=Mt-d;
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydus halys
pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Gloydus.
OX NCB1_TaxID=8714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=brevicaudus; TISSUE=Venom;
RX MEDLINE=99337693; PubMed=10406963;
RA Jeon O.H., Kim D.S.;
RT "Molecular cloning and functional characterization of a snake venom
metalloprotease.";
RU Eur. J. Biochem. 263:526-533 (1999).
DR EMBL; AF051789; AAD02654.1; -.
DR HSP; P18619; 1FVL.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
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DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; Disintegrin.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MERPO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KM Metalloprotease; Protease.
SQ SEQUENCE 482 AA; 53409 MW; C6014BBE87BC8B15 CRC64;

Query Match
Best Local Similarity 98.4%; Score 426; DB 2; Length 482;
Pred. No. 9.1e-35;
Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAGEBCDDGAPNPCCDAATCTLRPGACCAEGLCCDQCRFMKEGTCRMARGDDMDYCN 60
DB 410 EAGEBCDDGAPNPCCDAATCTLRPGACCAEGLCCDQCRFMKEGTCRMARGDDMDYCN 469
QY 61 GISACCPNPFHA 73
DB 470 GISACCPNPFHA 482

RESULT 4
Q80124 PRELIMINARY; PRT; 77 AA.
AC Q80124;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Disintegrin (Fragment).
OS Bothrops alternatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCB1_TaxID=64174;
RN [1]
RP SEQUENCE FROM N.A.
RA Ramos O.H.P., Selistre-de-Araujo H.S.;
RU Submitted (MAR-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY259516; MA075107.1; -.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR InterPro; IPR001762; Disintegrin.
DR Pfam; PF00200; Disintegrin; 1.
DR PRINTS; PR00289; Disintegrin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
KM Integrin.
FT NON_TER
SQ SEQUENCE 77 AA; 8179 MW; 680501C267ED496 CRC64;

Query Match
Best Local Similarity 97.0%; Score 420; DB 2; Length 77;
Pred. No. 7.5e-35;
Matches 69; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAGEBCDDGAPNPCCDAATCTLRPGACCAEGLCCDQCRFMKEGTCRMARGDDMDYCN 60
DB 5 EAGEBCDDGAPNPCCDAATCTLRPGACCAEGLCCDQCRFMKEGTCRMARGDDMDYCN 64
QY 61 GISACCPNPFHA 73
DB 65 GISACCPNPFHA 77

RESULT 5
Q7S2D5 PRELIMINARY; PRT; 73 AA.
AC Q7S2D5;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
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DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DS Disintegrin (Fragment).
 OS Agkistrodon calliginosus (Korean viper) (Gloydius ussuriensis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydius.
 CX NCBI_TaxID=35671;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Snake venom gland;
 RA Sun D.-U., Yang T.-S.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY204249; AAP20644.1;
 DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
 DR InterPro; IPR01762; Disintegrin.
 DR Pfam; PF00200; Disintegrin; 1.
 DR ProDom; PD000664; Disintegrin; 1.
 DR SMART; SM00050; DISIN; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; 1.
 DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 KW Integrin.
 SQ SEQUENCE 73 AA; 7768 MW; 615509DF966882EF CRC64;
 FT NON TER 1 1
 Query Match 94.7%; Score 410; DB 2; Length 73;
 Best Local Similarity 91.8%; Pred. No. 7.2e-34;
 Matches 67; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EAGEECDCGAPANPCCDATCTLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 60
 DB 1 EAGEECDCDSGNPCCDATCTLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 60
 QY 61 GISAGCPRPFFHA 73
 DB 61 GISAGCPRPFFHA 73
 RESULT 6
 ID 078ZD9 PRELIMINARY; PRT; 478 AA.
 AC 078ZD9;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DS Metalloprotease/disintegrin ussuriin
 OS Agkistrodon calliginosus (Korean viper) (Gloydius ussuriensis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydius.
 CX NCBI_TaxID=35671;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Snake venom gland;
 RA Sun D.-U., Yang T.-S.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY204245; AAP20640.1;
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
 DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR001590; Peptidase_M12B.
 DR InterPro; IPR002870; Peptidase_M12B_N.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF00200; Disintegrin; 1.
 DR Pfam; PF01562; Pept_M12B_propep; 1.
 DR Pfam; PF01421; Repolysin; 1.
 DR ProDom; PD000664; Disintegrin; 1.
 DR SMART; SM00050; DISIN; 1.
 DR PROSITE; PS50215; ADAM_MEPRO; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; 1.
 DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
 KW Integrin.

SQ SEQUENCE 478 AA; 53443 MW; CD2FBC975F62A771 CRC64;
 Query Match 94.7%; Score 410; DB 2; Length 478;
 Best Local Similarity 91.8%; Pred. No. 3.7e-33;
 Matches 67; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EAGEECDCGAPANPCCDATCTLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 60
 DB 406 EAGEECDCDSGNPCCDATCTLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 465
 QY 61 GISAGCPRPFFHA 73
 DB 466 GISAGCPRPFFHA 478
 RESULT 7
 ID 078CP2 PRELIMINARY; PRT; 105 AA.
 AC 078CP2;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DS Platelet aggregation inhibitor disintegrin (Fragment).
 GN Name=slimosin;
 OS Agkistrodon halys brevicaudus (Korean siamasa snake) (Gloydius halys brevicaudus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydius.
 CX NCBI_TaxID=259325;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kang I.C., Chung K.H., Lee S.U., Yun Y.D., Moon H.M., Kim D.S.;
 RT Purification and molecular cloning of a platelet aggregation
 RT inhibitor from the snake (Agkistrodon halys brevicaudus) venom.";
 RL Thromb. Res. 0:0-0(1998).
 DR EMBL; AF054626; AAC08997.1;
 DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR000519; P_Trefoil.
 DR Pfam; PF00200; Disintegrin; 1.
 DR PRINTS; PR00680; PTFREFOIL.
 DR ProDom; PD000664; Disintegrin; 1.
 DR SMART; SM00050; DISIN; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; 1.
 DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 KW Integrin.
 FT NON TER 1 1
 SQ SEQUENCE 105 AA; 11407 MW; 6F10AD4496D35F2 CRC64;
 Query Match 94.5%; Score 409; DB 2; Length 105;
 Best Local Similarity 93.2%; Pred. No. 1.2e-33;
 Matches 68; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EAGEECDCGAPANPCCDATCTLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 60
 DB 33 EAGEECDCDSGNPCCDATCTLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 92
 QY 61 GISAGCPRPFFHA 73
 DB 93 GISAGCPRPFFHA 105
 RESULT 8
 ID 090WC0 PRELIMINARY; PRT; 317 AA.
 AC 090WC0;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DS Metalloprotease (Fragment).
 GN Name=hxl-1;

OS Agkistrodon halys brevicaudus (Korean siamasa snake) (Gloydus halys brevicaudus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae; OC Viperidae; Crotalinae; Gloydus.
 OK NCBI_taxid=259325;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=venom gland;
 RA Xilian H.;
 RL Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF367868; AAK73517.1; --
 DR PIR; A59409; A59409.
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR001590; Peptidase_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF00200; Disintegrin; 1.
 DR Pfam; PF01421; Reptolysin; 1.
 DR PRINTS; PR00289; DISINTEGRIN.
 DR ProDom; PD000664; Disintegrin; 1.
 DR SMART; SM00050; DISIN; 1.
 DR PROSITE; PS50215; ADAM_MEPPO; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; 1.
 DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 317 AA; 35109 MW; 9851177BC3E2202E CRC64;

Query Match 94.5%; Score 409; DB 2; Length 317;
 Best Local Similarity 93.2%; Pred. No. 3.2e-33;
 Matches 68; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAGEECDCGAPANPCCDATCTLRPGACAGLCCDQCFMKEGTICMARGDMDYCN 60
 DB 245 EAGEECDCGSPNCPCCDATTCTLRPGACAGLCCDQCFMKEGTICMARGDMDYCN 304
 QY 61 GISACCPNPFHA 73
 DB 305 GISACCPNPFHA 317

RESULT 9
 Q98SP2 PRELIMINARY; PRT; 477 AA.
 ID 098SP2; PRELIMINARY; PRT; 477 AA.
 DT 01-UN-2001 (TRENBLrel. 17, Created)
 DT 01-UN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Bothrostatin.
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae; OC Viperidae; Crotalinae; Bothrops.
 OK NCBI_taxid=8724;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Silva C.A., Martins de Camargo A.C., de Toledo Serrano S.M.;
 RL Submitted (Feb-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF145931; AAK15542.1; --
 DR HSSP; P18619; 1FVL.
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR001590; Peptidase_M12B.
 DR InterPro; IPR002870; Peptidase_M12B_N.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF00200; Disintegrin; 1.
 DR Pfam; PF01562; Pep_M12B_propep; 1.
 DR Pfam; PF01421; Reptolysin; 1.
 DR PRINTS; PR00289; DISINTEGRIN.
 DR ProDom; PD000664; Disintegrin; 1.
 DR SMART; SM00050; DISIN; 1.
 DR PROSITE; PS50215; ADAM_MEPPO; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; 1.
 DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
 FT SIGNAL 1
 KW SIGNAL 18 Potential.
 FT CHAIN 190 391 Potential.
 FT CHAIN 392 480 Potential.
 SQ SEQUENCE 480 AA; 53619 MW; 5C95E6476511B3D7 CRC64;

Query Match 94.5%; Score 409; DB 2; Length 480;
 Best Local Similarity 91.8%; Pred. No. 4.6e-33;
 Matches 67; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAGEECDCGAPANPCCDATCTLRPGACAGLCCDQCFMKEGTICMARGDMDYCN 60

DR SMART; SM00050; DISIN; 1.
 DR PROSITE; PS50215; ADAM_MEPPO; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; 1.
 DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
 SQ SEQUENCE 477 AA; 53440 MW; AC973E8767E10B3 CRC64;

Query Match 94.5%; Score 409; DB 2; Length 477;
 Best Local Similarity 93.1%; Pred. No. 4.6e-33;
 Matches 67; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGEECDCGAPANPCCDATCTLRPGACAGLCCDQCFMKEGTICMARGDMDYCN 61
 DB 406 AGEECDCGSPNCPCCDATTCTLRPGACAGLCCDQCFMKEGTICMARGDMDYCN 465
 QY 62 ISAGCPNPFHA 73
 DB 466 ISAGCPNPFHA 477

RESULT 10
 Q90220 PRELIMINARY; PRT; 480 AA.
 ID Q90220; PRELIMINARY; PRT; 480 AA.
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Prepro-halystatin precursor.
 OS Agkistrodon halys pallasi (Chinese water moccasin) (Gloydus halys pallasi).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae; OC Viperidae; Crotalinae; Gloydus.
 OK NCBI_taxid=8714;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Fujisawa Y., Kuwoda S., Notoya K., Konishi H., Terashta Z.;
 RT "Halystatin, a novel disintegrin from agkistrodon halys, is a potent inhibitor of bone resorption and platelet aggregation."
 RT Takeda Kenkyusho Ho 53:39-56 (1994).
 RL EMBL; D28870; BAA06025.1; --
 DR EMBL; D28870; BAA06025.1; --
 DR PIR; A59410; A59410.
 DR PIR; A59411; A59411.
 DR HSSP; P18619; 1FVL.
 DR MEROPS; M12_134; --
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR001590; Peptidase_M12B.
 DR InterPro; IPR002870; Peptidase_M12B_N.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF00200; Disintegrin; 1.
 DR Pfam; PF01562; Pep_M12B_propep; 1.
 DR Pfam; PF01421; Reptolysin; 1.
 DR PRINTS; PR00289; DISINTEGRIN.
 DR ProDom; PD000664; Disintegrin; 1.
 DR SMART; SM00050; DISIN; 1.
 DR PROSITE; PS50215; ADAM_MEPPO; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; 1.
 DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
 FT SIGNAL 1
 KW SIGNAL 18 Potential.
 FT CHAIN 190 391 Potential.
 FT CHAIN 392 480 Potential.
 SQ SEQUENCE 480 AA; 53619 MW; 5C95E6476511B3D7 CRC64;

Query Match 94.5%; Score 409; DB 2; Length 480;
 Best Local Similarity 91.8%; Pred. No. 4.6e-33;
 Matches 67; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAGEECDCGAPANPCCDATCTLRPGACAGLCCDQCFMKEGTICMARGDMDYCN 60

Db 408 EAGEBCDGGSPNCCDAATCKLRGQAQCAEGLCCDDCRFMKGTVCRIARGDDMDYCN 467
QY 61 GISAGCPNPFHA 73
Db 468 GISAGCPNPFHA 480

RESULT 11
ID 073795 PRELIMINARY; PRT; 505 AA.
AC 073795.
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Metalloprotease.
GN Name=Mt-B;
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys pallas)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Gloydius.
OC NCBI_TaxID=8714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=brevicaudus; TISSUE=Venom;
RA Ueon O.H., Kim D.S.;
RL Submitted (Mar-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF051788; to the EMBL/GenBank/DBJ databases.
DR HSSP; P18619; 1FVL.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00200; Disintegrin_1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reptolysin_1.
DR PRINTS; PR00289; DISINTEGRIN.
DR PRODOM; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MERPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KM Metalloprotease; Protease.
SQ SEQUENCE 505 AA; 56336 MW; C96E99FC9C05378F CRC64;

Query Match 93.5%; Score 405; DB 2; Length 505;
Best Local Similarity 91.8%; Pred. No. 1.2e-32;
Matches 67; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPNCCDAATCKLRPQAQCAEGLCCDDCRFMKEGTCRMARGDDMDYCN 60
Db 433 EAGEBCDGGSPNCCDAATCKLRGQAQCAEGLCCDDCRFMKEGTICRGDDLDYCN 492

QY 61 GISAGCPNPFHA 73
Db 493 GISAGCPNPFHA 505

RESULT 12
DISI_AGRHA STANDARD; PRT; 71 AA.
AC P21858;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Disintegrin halysin (Platelet aggregation activation inhibitor).
OS Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;

OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=242054;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA MEDLINE=91362676; PubMed=1889330;
RA Huang T.-F., Yiu C.-S., Ouyang C.H., Teng C.-M.;
RT "Halysin, an antiplatelet Arg-Gly-Asp-containing snake venom peptide,
as fibrinogen receptor antagonist.";
RL Biochem. Pharmacol. 42:1209-1219(1991).
CC -1- FUNCTION: Inhibits fibrinogen interaction with platelet receptors
expressed on glycoprotein IIb-IIIa complex. Acts by binding to the
glycoprotein IIb-IIIa receptor on the platelet surface and
inhibits aggregation induced by ADP, thrombin, platelet-activating
factor and collagen.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
DR HSSP; P18619; 1FVL.
DR InterPro; IPR001762; Disintegrin.
DR Pfam; PF00200; Disintegrin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR PRODOM; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
KM Blood coagulation; Cell adhesion; Direct protein sequencing; Platelet.
FT DISULFID 47 66 By similarity.
FT SITE 51 53 Cell attachment site.
SQ SEQUENCE 71 AA; 7517 MW; E2B134B92715592 CRC64;

Query Match 91.7%; Score 397; DB 1; Length 71;
Best Local Similarity 91.5%; Pred. No. 1.4e-32;
Matches 65; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPNCCDAATCKLRPQAQCAEGLCCDDCRFMKEGTCRMARGDDMDYCN 60
Db 1 EAGEBCDGGSPNCCDAATCKLRGQAQCAEGLCCDDCRFMKGTVCRIARGDDMDYCN 60

QY 61 GISAGCPNPF 71
Db 61 GISAGCPNPF 71

RESULT 13
DISI_AGRPI STANDARD; PRT; 71 AA.
AC P16358;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Disintegrin aplysin (Platelet aggregation activation inhibitor).
OS Agkistrodon piscivorus piscivorus (Eastern cottonmouth).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=8716;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA MEDLINE=90046735; PubMed=2510158;
RA Chao B.H., Jakubowski U.A., Savage B., Ping Chow E., Marzec U.M.,
RA Harter U.A., Maraganore J.W.;
RT "Agkistrodon piscivorus piscivorus platelet aggregation inhibitor: a
potent inhibitor of platelet activation.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8050-8054(1989).
CC -1- FUNCTION: Inhibits fibrinogen interaction with platelet receptors
expressed on glycoprotein IIb-IIIa complex. Acts by binding to the
glycoprotein IIb-IIIa receptor on the platelet surface and
inhibits aggregation induced by ADP, thrombin, platelet-activating
factor and collagen.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -1- SIMILARITY: Belongs to the disintegrin family.
DR PIR: A33930, A3390.
DR HSP: P18619, 1FV.
DR InterPro: IPR001762; Disintegrin.
DR Pfam: PF00200; Disintegrin_1.
DR PRINTS: PR00289; DISINTEGRIN.
DR ProDom: PD000664; Disintegrin_1.
DR SMART: SM00050; DISIN: 1.
DR PROSITE: PS00427; DISINTEGRIN_1; 1.
DR PROSITE: PS50214; DISINTEGRIN_2; 1.
DR Blood coagulation; Cell adhesion; Direct protein sequencing; Platelet.
KM DISULFID 47 65 By similarity.
FT SITE 50 52 Cell attachment site.
SQ SEQUENCE 71 AA; 7522 MW; B514FDE47D67E266 CRC64;

Query Match 90.6%; Score 392.5; DB 1; Length 71;
Best Local Similarity 90.3%; Pred. No. 4e-32;
Matches 65; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 EAGEBDCGAPNPPCDATCKLRGACACAGLCCDQCFMKKEGTICRMAGDDMDPYCN 60
DB 1 EAGEBDCGSPENPCDADATCKLRGACAGLCCDQCFMKKEGTICRARGDVMNVCN 59
QY 61 GISACCPNPPH 72
DB 60 GISACCPNPPH 71

RESULT 14
DISG_TRIAB STANDARD; PRT; 73 AA.
AC P62384; P17496; (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last annotation update)
DE Disintegrin albolabrin (Platelet aggregation activation inhibitor).
OC Trimeresurus albolabris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Timereusurus.
OX NCBI_Taxid=8765;
RN [1]
RP TISSUE=Venom;
RC MEDLINE=90283463; PubMed=2191722;
RA Williams J., Kucinski B., Holt J., Niewiarowski S.;
RA "Elegantin and albolabrin purified peptides from viper venoms:
RT homologues with the RGD domain of fibrinogen and von Willebrand
RT factor";
RL Biochim. Biophys. Acta 1039:81-89(1990).
RN [2]
RP DISULFIDE BONDS.
RC TISSUE=Venom;
RC MEDLINE=91242430; PubMed=2036389;
RA Calvete J.J., Schaefer W., Soeska T., Lu W., Cook J.J., Jameson B.A.,
RA Niewiarowski S.;
RA "Identification of the disulfide bond pattern in albolabrin, an RGD-
RT containing peptide from the venom of Trimeresurus albolabris:
RT significance for the expression of platelet aggregation inhibitory
RT activity";
RL Biochemistry 30:5225-5229(1991).
RN [3]
RP STRUCTURE BY NMR.
RC MEDLINE=94109384; PubMed=8281937;
RA Jaseja M., Smith K.J., Lu X., Williams J.A., Trayer H., Trayer I.P.,
RA Hyde E.I.;
RA "1H-NMR studies and secondary structure of the RGD-containing snake
RT toxin, albolabrin";
RL Eur. J. Biochem. 218:853-860(1993).
RN [4]
RP STRUCTURE BY NMR.
RC MEDLINE=97052455; PubMed=8697089;
RA Smith K.J., Jaseja M., Lu X., Williams J.A., Hyde E.I., Trayer I.P.;

RT "three-dimensional structure of the RGD-containing snake toxin
RT albolabrin in solution, based on 1H NMR spectroscopy and simulated
RT annealing calculations";
RL Int. J. Pept. Protein Res. 48:220-228(1996).
CC -1- FUNCTION: Inhibits fibrinogen interaction with platelet receptors
CC expressed on glycoprotein IIb-IIIa complex. Acts by binding to the
CC glycoprotein IIb-IIIa receptor on the platelet surface and
CC inhibits aggregation induced by ADP, thrombin, platelet-activating
CC factor and collagen.
CC SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Belongs to the disintegrin family.
DR PIR: A23731, A23731.
DR HSP: P18619, 1FV.
DR InterPro: IPR001762; Disintegrin.
DR Pfam: PF00200; Disintegrin_1.
DR PRINTS: PR00289; DISINTEGRIN.
DR ProDom: PD000664; Disintegrin_1.
DR SMART: SM00050; DISIN: 1.
DR PROSITE: PS00427; DISINTEGRIN_1; 1.
DR PROSITE: PS50214; DISINTEGRIN_2; 1.
DR Blood coagulation; Cell adhesion; Direct protein sequencing; Platelet.
KM DISULFID 6 15 Probable.
FT DISULFID 8 16 Probable.
FT DISULFID 21 35 Probable.
FT DISULFID 29 59 Probable.
FT DISULFID 34 38 Probable.
FT DISULFID 47 66 Probable.
FT SITE 51 53 Cell attachment site.
SQ SEQUENCE 73 AA; 7573 MW; F7E011E2F46FEF14 CRC64;

Query Match 90.3%; Score 391; DB 1; Length 73;
Best Local Similarity 87.7%; Pred. No. 5.8e-32;
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEBDCGAPNPPCDATCKLRGACACAGLCCDQCFMKKEGTICRMAGDDMDPYCN 60
DB 1 EAGEBDCGSPENPCDADATCKLRGACAGLCCDQCFMKKEGTICRARGDVMNVCN 60
QY 61 GISACCPNPPH 73
DB 61 GISACCPNPPH 73

RESULT 15
DISG_TRIAB STANDARD; PRT; 73 AA.
AC P62383; P17496; (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last annotation update)
DE Disintegrin trigramin gamma (Platelet aggregation activation
DE inhibitor).
OC Trimeresurus gramineus (Indian green tree viper) (Green habu snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Timereusurus.
OX NCBI_Taxid=8767;
RN [1]
RP TISSUE=Venom;
RC MEDLINE=90207217; PubMed=2320569;
RA Dennis M.S., Henzel W.J., Pitti R.M., Lipari M.T., Napier M.A.,
RA Delisher T.A., Bunting S., Lazarus R.A.;
RA "Platelet glycoprotein IIb-IIIa protein antagonists from snake venoms:
RT evidence for a family of platelet aggregation inhibitors";
RL Proc. Natl. Acad. Sci. U.S.A. 87:2471-2475(1990).
CC -1- FUNCTION: Inhibits fibrinogen interaction with platelet receptors
CC expressed on glycoprotein IIb-IIIa complex. Acts by binding to the
CC glycoprotein IIb-IIIa receptor on the platelet surface and
CC inhibits aggregation induced by ADP, thrombin, platelet-activating
CC factor and collagen.
CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- SIMILARITY: Belongs to the disintegrin family.
 DR PIR: E35982; E35982.
 DR HSSP: P18619; 1FVL.
 DR InterPro: IPR001762; Disintegrin.
 DR Pfam: PF00200; Disintegrin_1.
 DR PRINTS: PR00289; DISINTEGRIN.
 DR ProDom: PD000664; Disintegrin; 1.
 DR SMART: SM00050; DISIN; 1.
 DR PROSITE: PS00427; DISINTEGRIN_1; 1.
 DR PROSITE: PS50214; DISINTEGRIN_2; 1.
 KW Blood coagulation; Cell adhesion; Direct protein sequencing; Platelet.
 FT DISULFID 6 15 By similarity.
 FT DISULFID 8 16 By similarity.
 FT DISULFID 21 35 By similarity.
 FT DISULFID 29 59 By similarity.
 FT DISULFID 34 38 By similarity.
 FT DISULFID 47 66 By similarity.
 FT STRB 51 53 Cell attachment site.
 SQ SEQUENCE 73 AA; 7573 MW; F7B01E2F46FEF14 CRC64;

Query Match 90.3%; Score 391; DB 1; Length 73;
 Best Local Similarity 87.7%; Pred. No. 5.8e-32;
 Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEECDCGAPANPCDAATCKLRPGAQCAAGLCCDCCRFMKESTICRMARGDDMDPYCN 60
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 EAGEDCCDGGSPANPCDAATCKLLPGAQCGEGLCDDCCSFMKKGTICRRARGDDLDYCN 60
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 GISAGCPRNPPHA 73
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 GISAGCPRNPPHA 73
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: December 3, 2004, 21:38:11
 Job time : 137 secs

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OW protein - protein search, using sw model

Run on: December 3, 2004, 20:08:42 ; Search time 116 Seconds

(without alignments)
225.752 Million cell updates/sec

Title: US-10-089-473a-1

Perfect score: 493
Sequence: 1 EAGEECDGAPANPCDAAAT.....DMDDYNGISAGCPNPFHA 73

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 segs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseq_23Sep04:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	433	100.0	73	5	AAE19787
2	409	94.5	73	2	AAW14083
3	409	94.5	73	5	AAV58231
4	409	94.5	73	5	AAE19791
5	409	94.5	480	2	AAK42867
6	402	92.8	73	2	AAK06494
7	392.5	90.6	71	5	AAU75225
8	391	90.3	73	2	AAK06395
9	391	90.3	73	2	AAK10106
10	391	90.3	73	2	AAK53946
11	391	90.3	73	2	AAW45500
12	391	90.3	73	2	ADH67966
13	391	90.3	73	3	ABE20598
14	391	90.3	73	5	ABG30392
15	391	90.3	73	7	ABU63163
16	391	90.3	73	8	ADM10975
17	390	90.1	96	2	AAK28703
18	390	90.1	96	2	AAK28707
19	390	90.1	97	2	AAK28704
20	390	90.1	97	2	AAK28706
21	390	90.1	99	2	AAK25153
22	390	90.1	99	2	AAK25149
23	390	90.1	106	2	AAK25148
24	390	90.1	106	2	AAK25152
25	387	89.4	97	2	AAK28705

26	387	89.4	97	2	AAK28708	AAK28708 Bifunctio
27	387	89.4	98	2	AAK25154	AAK25154 Bifunctio
28	387	89.4	98	2	AAK25150	AAK25150 Bifunctio
29	386.5	89.3	71	2	AAK53942	AAK53942 Bifunctio
30	384	88.7	96	2	AAK25151	AAK25151 Bifunctio
31	384	88.7	96	2	AAK25382	AAK25382 Bifunctio
32	384	88.7	96	2	AAK25147	AAK25147 Bifunctio
33	382	88.2	72	1	AAK91320	AAK91320 New trig
34	379	87.5	73	2	AAK10110	AAK10110 Trigramin
35	379	87.5	73	2	ADP65996	ADP65996 Snake ven
36	375	86.6	72	2	AAK10109	AAK10109 Trigramin
37	372.5	86.0	71	2	ADP66000	ADP66000 Snake ven
38	371.5	85.8	71	2	AAK53937	AAK53937 Disintegr
39	371	85.7	72	2	ADP65998	ADP65998 Snake ven
40	368	85.0	483	3	AAV79413	AAV79413 Southern
41	368	85.0	483	4	AAE03036	AAE03036 Agkistrod
42	360	83.1	478	5	ABG70857	ABG70857 Disintegr
43	356	82.2	72	2	AAK46215	AAK46215 Snake ven
44	356	82.2	72	2	AAK46218	AAK46218 Snake ven
45	356	82.2	72	2	AAW50453	AAW50453 Snake ven

ALIGNMENTS

RESULT 1	AAE19787	AAE19787 standard; protein; 73 AA.
ID	AAE19787	
XX	AAE19787	
AC	AAE19787	
XX		
DT	29-AUG-2003	(revised)
DT	07-AUG-2003	(revised)
DT	18-JUN-2002	(first entry)
XX		
DE	Agkistrodon saxatilis emelianov saxatillin protein.	
XX		
KW	Korean snake; saxatillin; anticoagulant; cytostatic; venom; anti-tumour;	
KW	platelet aggregation; angiogenesis; cytotoxicity.	
OS	Gloydius halys.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 1..3	
FT		note="Encoded by GGA"
XX		
PN	WO200214488-A1.	
XX		
PD	21-FEB-2002.	
XX		
PF	26-JUL-2000; 2000WO-KR000809.	
XX		
PR	26-JUL-2000; 2000WO-KR000809.	
XX		
PA	(CHUN/) CHUNG K.	
PA	(KIMD/) KIM D.	
XX		
PI	Hong S, Koh Y, Sohn Y, You W, Jang Y, Huh C;	
DR	WPI, 2002-241903/29.	
DR	N-PSDB; AAD31060.	
XX		
PT	New CDNA encoding Saxatillin protein derived from venom of Korean snake	
PT	Agkistrodon saxatilis emelianov, useful as anti-platelet aggregation	
PT	agent and anti-tumor agent.	
XX		
PS	Claim 2; Page 35; 41pp; English.	
XX		
CC	The invention relates to a CDNA encoding Saxatillin protein derived from	
CC	venom of Korean snake Agkistrodon saxatilis emelianov. The CDNA is useful	
CC	for as an anti-tumour agent and for effectively suppressing platelet	
CC	aggregation which makes it possible as and an active ingredient of anti-	
CC	platelet agent. Saxatillin is useful for inhibiting angiogenesis induced	

CC by tumour and for inhibiting tumour without cytotoxicity. The present
 CC sequence is Agkistrodon saxatilis emeljanov saxatilis protein. (Updated
 CC on 07-AUG-2003 to correct OS field.) (Updated on 29-AUG-2003 to
 CC standardise OS field)

XX Sequence 73 AA;

Query Match 100.0%; Score 433; DB 5; Length 73;
 Best Local Similarity 100.0%; Pred. No. 9.2e-32;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPNPCCDAATCTLRPGACAGELCCDQCRFMKEGTICRMARGDDMDYCN 60
 DB 1 EAGEBCDGGAPNPCCDAATCTLRPGACAGELCCDQCRFMKEGTICRMARGDDMDYCN 60
 QY 61 GISAGCPNPFHA 73
 DB 61 GISAGCPNPFHA 73

RESULT 2
 AAM14083
 ID AAM14083 standard; peptide; 73 AA.

AC AAM14083;
 DT 17-OCT-2003 (revised)
 DT 27-OCT-1997 (first entry)

DE Platelet aggregation inhibitor, Salmosin.

KM Salmosin; inhibits; blood; platelet aggregation; venom; Korean;
 KM salmosa viper; Agkistrodon halys brevicaudus; treatment; thrombosis.

XX Gloydius halys brevicaudus.

XX FR2736266-A1.

XX 10-JAN-1997.

XX 24-AUG-1995; 95FR-00010049.

XX 05-JUL-1995; 95KR-00019685.

XX (MOGA-) MOGAM BIOTECHNOLOGY RES INST.

PI In CK, Kwang HC, Soo JL, Deo SK, Hak DK, Yung DY, Jeong HY;
 PI Hong KM;

DR WPI; 1997-121376/12.

PT Peptide derived from Korean salmosa viper venom - useful as blood
 PT platelet aggregation inhibitor, for the management of thrombosis.

XX Claim 1; Page 11; 15pp; French.

CC This peptide, designated Salmosin, inhibits blood platelet aggregation.
 CC It is derived from the venom of the Korean salmosa viper (Agkistrodon
 CC halys brevicaudus). Salmosin can be used, in particular, in compositions
 CC for management of thrombosis. Salmosin also has higher activity than
 CC kistrin, gamma-triglycamin and echistatin. (Updated on 17-OCT-2003 to
 CC standardise OS field)

XX Sequence 73 AA;

Query Match 94.5%; Score 409; DB 2; Length 73;
 Best Local Similarity 93.2%; Pred. No. 1.3e-29;
 Matches 68; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPNPCCDAATCTLRPGACAGELCCDQCRFMKEGTICRMARGDDMDYCN 60
 DB 1 EAGEBCDGGAPNPCCDAATCTLRPGACAGELCCDQCRFMKEGTICRMARGDDMDYCN 60

QY 61 GISAGCPNPFHA 73
 DB 61 GISAGCPNPFHA 73

RESULT 3
 AAY58231
 ID AAY58231 standard; protein; 73 AA.

AC AAY58231;

DT 12-SEP-2003 (revised)
 DT 27-MAR-2000 (first entry)

DE Korean snake venom salmosin.

KM Salmosin; angiogenesis; inhibitor; integrin; antagonist; disintegrin;
 KM metastasis; cancer; tumour.

XX Gloydius halys.

FT Key Location/Qualifiers
 FT Region 51..53
 FT /note="RGD motif"

PN EP667276-A2.

XX 29-DEC-1999.

XX 23-JUN-1999; 99EP-00304935.

PR 23-JUN-1998; 98KR-00023778.
 PR 04-JUN-1999; 99KR-00020579.

XX (KIMD/) KIM D.

XX Kim D, Chung KH, Kang I;

XX WPI: 2000-064611/06.

XX N-PSDB; AAZ55609.

PT Novel polypeptides used for antitumor therapy.

PS Claim 1; Page 13; 24pp; English.

CC This sequence represents a 7.5 kD salmosin protein of a Korean snake,
 CC Agkistrodon halys brevicaudus. Salmosin is a disintegrin, a family of
 CC small proteins mainly derived from snake venom which contain an RGD or
 CC RGD motif (the structural motif recognised by platelet fibrinogen
 CC receptor alpha-2-b-beta-3). Disintegrins act as potent antagonists of
 CC several integrins including alpha-v-beta-3 and alpha-5-beta-1 integrins,
 CC the former being a marker of angiogenic blood vessels and certain
 CC malignant cells. Disintegrins inhibit tumour metastasis by blocking
 CC tumour cell adhesion to the extracellular matrix, and antagonism of
 CC integrin alpha-v-beta-3 can suppress tumour-induced angiogenesis.
 CC Salmosin can be used as an anticancer agent. It may be used for the
 CC inhibition or reduction of tumour cell angiogenesis, the inhibition of
 CC metastatic tumour formation and the inhibition or reduction of metastatic
 CC tumour growth. Nucleotides encoding salmosin may be used in gene therapy
 CC applications. Many types of cancer may be treated with salmosin or
 CC nucleotides encoding it, including leukemia and cancers of the breast,
 CC ovary, uterus, skin, lung, larynx, colon, pancreas, testis, liver, brain,
 CC muscle and bone. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 73 AA;

Query Match 94.5%; Score 409; DB 3; Length 73;
 Best Local Similarity 93.2%; Pred. No. 1.3e-29;
 Matches 68; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPNPCCDAATCTLRPGACAGELCCDQCRFMKEGTICRMARGDDMDYCN 60
 DB 1 EAGEBCDGGAPNPCCDAATCTLRPGACAGELCCDQCRFMKEGTICRMARGDDMDYCN 60

OY 61 GISAGCPNPFHA 73
 DB 61 GISAGCPNPFHA 73

RESULT 4
 AAE19791
 ID AAE19791 standard; protein; 73 AA.

XX AC AAE19791;
 XX DT 29-AUG-2003 (revised)
 XX DT 18-JUN-2002 (first entry)
 XX DE Agkistrodon halys brevicaudus salmosin protein.

XX KM Korean snake; saxatillin; anticoagulant; cytostatic; venom; anti-tumour;
 XX KM platelet aggregation; angiogenesis; salmosin; cytotoxicity.

XX OS Gloydius halys brevicaudus.

XX PN WO200214488-A1.

XX PD 21-FEB-2002.

XX PF 26-JUL-2000; 2000WO-KR000809.

XX PR 26-JUL-2000; 2000WO-KR000809.

XX PA (CHUN/) CHUNG K.

XX PA (KIMD/) KIM D.

XX PI Hong S, Koh Y, Sohn Y, You W, Jang Y, Huh C;

XX DR WPI; 2002-241903/29.

XX PT New cDNA encoding Saxatillin protein derived from venom of Korean snake
 XX PT Agkistrodon saxatilis emelianov, useful as anti-platelet aggregation
 XX PT agent and anti-tumor agent.

XX PS Example 5; Page 38-39; 41pp; English.

XX CC The invention relates to a cDNA encoding Saxatillin protein derived from
 CC CC venom of Korean snake Agkistrodon saxatilis emelianov. The cDNA is useful
 CC CC for as an anti-tumour agent and for effectively suppressing platelet
 CC CC aggregation which makes it possible as and an active ingredient of anti-
 CC CC platelet agent. Saxatillin is useful for inhibiting angiogenesis induced
 CC CC by tumour and for inhibiting tumour without cytotoxicity. The present
 CC CC sequence is Agkistrodon halys brevicaudus salmosin protein. (updated on
 CC CC 29-AUG-2003 to standardise OS field)

XX SQ Sequence 73 AA;

Query Match 94.5%; Score 409; DB 5; Length 73;
 Best Local Similarity 93.2%; Pred. No. 1.3e-29;
 Matches 68; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 EAGEBCDCCGAPNCCDAATCKLRPGAQCAEGLCCDCCRFMKGGTTCRMARGDMDYCN 60
 DB 1 EAGEBCDCCGSPGNPCDAATCKLRGAQCAEGLCCDCCRFMKGGTTCRRARGDMDYCN 60

OY 61 GISAGCPNPFHA 73
 DB 61 GISAGCPNPFHA 73

RESULT 5
 AAR42867
 ID AAR42867 standard; protein; 480 AA.

XX AC AAR42867;
 XX XX

DT 24-OCT-2003 (revised)
 DT 11-MAY-1994 (first entry)

XX DE Platelet aggregation inhibitory peptide.

XX KM Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF.

XX OS Gloydius halys blomhoffi.

XX PN JP05255395-A.

XX PD 05-OCT-1993.

XX PF 03-OCT-1991; 91UP-00256234.

XX PR 26-OCT-1990; 90UP-00287116.

XX PR 20-FEB-1991; 91UP-00026328.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX DR WPI; 1993-348481/44.

XX DR N-PSDB; AAG50394.

XX PT Polypeptide of specified aminoacid sequence - used for inhibiting
 XX PT platelet aggregation caused by e.g. collagen, thrombin, etc.
 XX PS Example; Page 33-35; 50pp; Japanese.

XX CC The sequence is that of a polypeptide which inhibits platelet aggregation
 CC CC caused by ADP, collagen, thrombin, arachidonic acid and PAF. (updated on
 CC CC 24-OCT-2003 to standardise OS field)

XX SQ Sequence 480 AA;

Query Match 94.5%; Score 409; DB 2; Length 480;
 Best Local Similarity 91.8%; Pred. No. 6.5e-29;
 Matches 67; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 EAGEBCDCCGAPNCCDAATCKLRPGAQCAEGLCCDCCRFMKGGTTCRMARGDMDYCN 60
 DB 408 EAGEBCDCCGSPGNPCDAATCKLRGAQCAEGLCCDCCRFMKGGTTCRRARGDMDYCN 467

OY 61 GISAGCPNPFHA 73
 DB 468 GISAGCPNPFHA 480

RESULT 6
 AAR06494
 ID AAR06494 standard; protein; 73 AA.

XX AC AAR06494;

XX DT 25-MAR-2003 (revised)

XX DT 04-JAN-1991 (first entry)

XX DE Platelet aggregation inhibitor.

XX KM Snake venom; thromboxan A2; thrombosis; anti-coagulant.

XX OS Synthetic.

XX PN WO9008772-A.

XX PD 09-AUG-1990.

XX PF 27-JAN-1989; 89US-00303585.

XX PR 27-JAN-1989; 89US-00303585.

XX PR 01-NOV-1989; 89US-00430313.

XX PA (UYBO-) UNIV BOSTON.

PA (BIOJ) BIOGEN INC.
 XX Maraganore J, Jakubowski J, Chao B;
 XX WPI, 1990-260891/34.
 DR N-BSDB; AA005730.
 XX
 PT Pure platelet activation inhibiting polypeptide from snake venom - used
 PT for preventing agglutination and release in vivo or vitro, and new
 PT recombinant dna encoding it.
 XX
 PS Claim 3; Fig 9; 73pp; English.
 XX
 CC The sequence is deduced from the coding strand of a synthetic gene for a
 CC polypeptide inhibitor of platelet activation. The polypeptide is
 CC analogous to that obtd. from the venom of Agkistrodon p. piscivorus
 CC (North American Water Moccasin). The gene can be used to produce
 CC recombinant inhibitor or fusion proteins with eg. hirudin derivs. These
 CC can be used to decrease/ inhibit platelet aggregation and release in vivo
 CC or in vitro. Usual dose is 0.01-100 mg/kg body wt. The recombinant
 CC device can also be used to coat the surfaces of invasive medical
 CC devices. It can also block stenosis and spasm at the site of thrombosis (
 CC by inhibiting the release of thromboxan A2). See also AAR06508. (Updated
 CC on 25-MAR-2003 to correct PA field.)
 CC
 SO Sequence 73 AA;
 Query Match 92.8%; Score 402; DB 2; Length 73;
 Best Local Similarity 90.3%; Pred. No. 5.7e-29;
 Matches 65; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EAGEECDCGAPANPCDDATCTLRGACCAEGLCDDCFMKKEGTICRMARAGDDMDVDCN 60
 DB 2 EAGEECDCGSPNPFCDATCTLRGACCAEGLCDDCFMKKEGTICRRARAGDDVNDYCN 61
 QY 61 GISAGCPNPNPF 72
 DB 62 GISAGCPNPNPF 73
 RESULT 7
 AAU75225
 ID AAU75225 standard; protein; 71 AA.
 AC AAU75225;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Agkistrodon piscivorus protein #2 relating to albumin fusion proteins.
 XX
 KW Albumin fusion protein; therapeutic protein; immune disorder;
 KW autoimmune disorder; blood-related disorder; hyperproliferative disorder;
 KW renal disorder; cardiovascular disorder; respiratory disorder;
 KW neurological disorder; endocrine disorder; reproductive system disorder;
 KW gastrointestinal disorder; infectious disease; wound healing;
 KW human serum albumin; HSA; HA.
 XX
 OS Agkistrodon piscivorus.
 XX
 PN WO200179271-A1.
 XX
 PD 25-OCT-2001.
 XX
 PF 12-APR-2001; 2001WO-US012009.
 XX
 PR 12-APR-2000; 2000US-0229358P.
 PR 25-APR-2000; 2000US-0199384P.
 PR 21-DEC-2000; 2000US-0256931P.
 XX
 PA (PRIN-) PRINCIPAL PHARM CORP.
 PA (DELZ) DELTA BIOTECHNOLOGY LTD.
 XX
 PI Balance DJ, Sleep D, Turner AJ, Sadeghi H, Prior CP;

XX
 DR WPI; 2002-179329/23.
 XX
 PT New albumin fusion proteins with extended shelf life, useful for treating
 PT leukemia, warts, hepatitis, multiple sclerosis and AIDS, comprises
 PT therapeutic protein fused to albumin.
 XX
 PS Disclosure; Page 336; 338pp; English.
 XX
 CC The present invention relates to albumin fusion proteins comprising a
 CC therapeutic protein and albumin (e.g. human serum albumin (HSA or HA)).
 CC The albumin fusion proteins are useful for treating, preventing, or
 CC ameliorating various disorders. Such disorders include immune disorders,
 CC autoimmune disorders, blood-related disorders, hyperproliferative
 CC disorders, renal disorders, cardiovascular disorders, respiratory
 CC disorders, neurological disorders, endocrine disorders, reproductive
 CC system disorders, gastrointestinal disorders, infectious disease, and
 CC wound healing. Therapeutic proteins can be stabilised to extend shelf
 CC life and/or retain the protein's activity for extended periods of time in
 CC solution, in vivo or in vitro by genetically or chemically fusing the
 CC protein to albumin or its fragment or variant. In addition the use of
 CC albumin fusion proteins reduces the need to formulate protein solutions
 CC with large excesses of carrier proteins to prevent loss of therapeutic
 CC protein due to factors such as binding to the container. The extension of
 CC shelf life was tested by measuring biological activity (Nb2 cell
 CC proliferation) of human albumin-human growth hormone (HA-hGH) fusion
 CC protein remaining after incubation in cell culture media for up to 3
 CC weeks. At week 3 there was still approximately 95% cell proliferation
 CC compared to no activity of unused hGH. The present sequence represents
 CC an Agkistrodon piscivorus protein of unknown function. Note: The present
 CC sequence is given in the sequence listing but is not mentioned elsewhere
 CC in the specification
 CC
 SO Sequence 71 AA;
 Query Match 90.6%; Score 392.5; DB 5; Length 71;
 Best Local Similarity 90.3%; Pred. No. 4e-28;
 Matches 65; Conservative 5; Mismatches 1; Indels 1; Gaps 1;
 QY 1 EAGEECDCGAPANPCDDATCTLRGACCAEGLCDDCFMKKEGTICRMARAGDDMDVDCN 60
 DB 1 EAGEECDCGSPNPFCDATCTLRGACCAEGLCDDCFMKKEGTICRRARAGDDVNDYCN 59
 QY 61 GISAGCPNPNPF 72
 DB 60 GISAGCPNPNPF 71
 RESULT 8
 AAR06395
 ID AAR06395 standard; protein; 73 AA.
 AC AAR06395;
 XX
 DT 25-MAR-2003 (revised)
 DT 13-DEC-1990 (first entry)
 XX
 DE Albolabrin.
 XX
 KW Fibrinogen binding; inhibitor; platelet aggregation; thrombosis;
 KW Viper venom.
 XX
 OS Trimeresurus albolabris.
 XX
 PN EP382451-A.
 XX
 PD 16-AUG-1990.
 XX
 PF 05-FEB-1990; 90EP-00301181.
 XX
 PR 07-FEB-1989; 89US-00307642.
 XX
 PA (MERI) MERCK & CO INC.

PA (UTEM) UNIV TEMPLE.
PA (FRIE/) FRIEDMAN P A.
XX Friedmann PA, Jacobs JW, Gould RJ, Polokoff MA, Gan ZR;
PI Niewiatows S, Holt JC, Rucinski B;
XX WPI, 1990-248351/33.
DR
XX
XX Viper venom polypeptide(s) - useful for inhibiting fibrinogen binding to
PT human platelets and inhibiting fibrinogen-induced aggregation.
XX
XX
XX Claim 2; Page 13; 13pp; English.
XX
XX The peptide is prep. from the venom of the viper T. albolabris or may be
CC prep. by genetic engineering or solid phase synthesis. It inhibits both
CC fibrin binding to human platelets and fibrinogen-induced aggregation of
CC human platelets. It is eliminated from the circulation rapidly and is
CC therefore useful in situations where a strong antithrombotic action of
CC short duration is needed, e.g. in surgery on peripheral arteries, in
CC cardiovascular surgery and the interaction of platelets with artificial
CC surfaces. See also AAR06389-97. (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
XX
SQ Sequence 73 AA;
XX
XX
XX Query Match 90.3%; Score 391; DB 2; Length 73;
Best Local Similarity 87.7%; Pred. No. 5.6e-28;
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
OY 1 EAGEBCDCCGAPANPCDDAATCKLRPGACAGELCCDQCFMKETICRMARGDDMDYCN 60
DB 1 EAGEBCDCCGAPANPCDDAATCKLRPGACAGELCCDQCFMKETICRMARGDDMDYCN 60
OY 61 GISAGCPRNPFHA 73
DB 61 GISAGCPRNPLHA 73
XX
XX
XX RESULT 9
AAR10106
ID AAR10106 standard; protein; 73 AA.
XX
XX AAR10106;
AC
XX
XX 13-MAR-1991 (first entry)
DT
XX
XX Trigramin-gamma.
DE
XX
XX Platelet aggregation inhibitor; snake venom; fibrin binding; inhibition;
KM GP IIA; GP IIA; hypercoagulation.
XX
XX
XX Synthetic.
OS
XX
XX WO9015072-A.
PN
XX
XX 13-DEC-1990.
PD
XX
XX 07-JUN-1989; 89US-00362718.
PF
XX
XX 07-JUN-1989; 89US-00362718.
FR
XX
XX 07-JUN-1989; 89US-00362718.
PA (GETH) GENENTECH INC.
XX
XX
XX Lazarus R, Dennis M;
PI
XX
XX WPI, 1991-007159/01.
DR
XX
XX N-PSDB; AAO10160.
DR
XX
XX Platelet aggregation inhibiting amino acid sequences - are derived from
PT snake venom and inhibit fibrinogen binding to GP IIA-GP IIA.
XX
XX
XX Disclosure; Fig 1; 91pp; English.
XX

CC The sequence was produced by recombinant techniques using a synthetic
CC gene prep. from 10 oligonucleotides based on the amino acid sequence
CC determined by Edman degradation. The recombinant trigramin-gamma is used
CC in treatment of hypercoagulation-related states. See also AAR10107-R10113
XX
XX
SQ Sequence 73 AA;
XX
XX
XX Query Match 90.3%; Score 391; DB 2; Length 73;
Best Local Similarity 87.7%; Pred. No. 5.6e-28;
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
OY 1 EAGEBCDCCGAPANPCDDAATCKLRPGACAGELCCDQCFMKETICRMARGDDMDYCN 60
DB 1 EAGEBCDCCGAPANPCDDAATCKLRPGACAGELCCDQCFMKETICRMARGDDMDYCN 60
OY 61 GISAGCPRNPFHA 73
DB 61 GISAGCPRNPLHA 73
XX
XX
XX RESULT 10
AAR53946
ID AAR53946 standard; peptide; 73 AA.
XX
XX
XX AAR53946;
AC
XX
XX 27-AUG-2003 (revised)
DT
XX
XX 25-MAR-2003 (revised)
DT
XX
XX 21-DEC-1994 (first entry)
DT
XX
XX Distintegrin peptide #14.
DE
XX
XX Distintegrin; Viperidae; snake; integrin; inhibitor; fibrinogen;
KM integrin binding sites; GP IIB/IIA; human; platelets; radiolabel;
KM treatment; diagnosis; venous; arterial; thrombi; pulmonary emboli;
KM tumours; abscesses; thrombus component.
XX
XX
XX Trimeresurus albolabris.
OS
XX
XX WO9409036-A1.
PN
XX
XX 28-APR-1994.
PD
XX
XX
PF 05-OCT-1993; 93WO-US009523.
PR
XX
XX 19-OCT-1992; 92US-00965674.
PR
XX
XX (UTEM) UNIV TEMPLE.
PA
XX
XX Knight LC, Maurer AH;
PI
XX
XX WPI, 1994-151248/18.
DR
XX
XX
XX Radio-labelled polypeptide(s) derived from Viperidae disintegrin(s) - for
PT treatment and diagnosis of venous and arterial thrombi, pulmonary emboli
and tumours or abscesses having a thrombus component.
XX
XX
XX Claim 28; Page 48; 62pp; English.
XX
XX
XX The sequences given in AAR53933-46 are disintegrin peptides. Disintegrins
CC are low molecular weight proteins from the Viperidae family of snakes
CC which bind integrin proteins similar to the endogenous messenger and
CC structurally interactive molecules. Disintegrins are competitive
CC inhibitors of biomolecules, such as fibrinogen, for integrin binding
CC sites such as GP IIB/IIA on human platelets. Disintegrins contain the
CC tripeptide sequence Arg-Gly-Asp. Radiolabelled disintegrin peptides can
CC be used for the treatment and diagnosis of venous and arterial thrombi,
CC pulmonary emboli and tumours or abscesses that have a thrombus component.
CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
XX
XX Sequence 73 AA;
XX

Query Match 90.3%; Score 391; DB 2; Length 73;
Best Local Similarity 87.7%; Pred. No. 5,6e-28;
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEBDCGAPNPPCCDAATCTLRPGACCAAGLCCDQCFMKKEGTTCMARGDMDYCN 60
DB 1 EAGEBDCGSPNPPCCDAATCTLRPGACCGELCCDQCSFMKKGITICRRAGDDLDYCN 60

OY 61 GISAGCFRNPFFHA 73
DB 61 GISAGCFRNPFFHA 73

RESULT 11
AAM45500
ID AAM45500 standard; peptide; 73 AA.

AC AAM45500;

DT 20-MAY-1998 (first entry)

DE Albolabrin peptide targeting ligand.

KM Contrast agent; targeted composition; diagnosis; diseased tissue;

KW glycoprotein GPIIb/IIIa receptor; albolabrin.

OS Synthetic.

PN WO9640285-A1.

PD 19-DEC-1996.

PF 06-JUN-1996; 96WO-US009938.

PR 07-JUN-1995; 95US-00497684.

PR 01-MAY-1996; 96US-00640464.

PA (IMAR-) IMARX PHARM CORP.

PI Unger EC, Shen D, Wu G;

DR WPI; 1997-077233/07.

PT Contrast agent or targeted compsn. for imaging or treating diseased
PT tissue - comprising lipid, protein or polymer, a gas, and a targeting
PT ligand e.g. a protein, peptide, saccharide or steroid.

PS Disclosure; Page 57; 175pp; English.

CC This sequence represents a targeting ligand. The invention relates to a
CC contrast agent for diagnostic imaging or a target composition which
CC comprises: (i) a lipid, protein or polymer and (ii) a gas, in combination
CC with (iii) a targeting ligand (TL). TL targets cells or receptors
CC selected from myocardial, endothelial, epithelial and tumour cells and
CC the glycoprotein GPIIb/IIIa receptor. Also claimed are: a composition
CC comprising vesicles containing (i) - (iii) and an aqueous carrier; a
CC targeted vesicle composition comprising a fluorinated gas and a targeting
CC ligand (TL) which targets tissues or receptors; a formulation for
CC therapeutic or diagnostic use comprising (i)-(iii) and a bioactive agent;
CC and a method for providing an image of an internal region of a patient,
CC or for diagnosing the presence of diseased tissue comprising: (a)
CC administration of a composition as above; and (b) scanning the patient
CC using ultrasound to obtain a visible image of the region of diseased
CC tissue. The methods and compounds are useful for imaging or diagnosing
CC the presence of diseased tissue, especially myocardial, endothelial or
CC epithelial tissue but also gastrointestinal and cardiovascular regions.
CC In particular the ligand targets regions of arteriosclerosis. Stabilised
CC vesicles are particularly useful for perfusion imaging. The vesicles may
CC also be used to deliver active agents to an intended target such as
CC tissue or a receptor, and ultrasound can then be used to promote rupture
CC of the vesicles and release a bioactive or diagnostic agent

CC Sequence 73 AA;

Query Match 90.3%; Score 391; DB 2; Length 73;
Best Local Similarity 87.7%; Pred. No. 5,6e-28;
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEBDCGAPNPPCCDAATCTLRPGACCAAGLCCDQCFMKKEGTTCMARGDMDYCN 60
DB 1 EAGEBDCGSPNPPCCDAATCTLRPGACCGELCCDQCSFMKKGITICRRAGDDLDYCN 60

OY 61 GISAGCFRNPFFHA 73
DB 61 GISAGCFRNPFFHA 73

RESULT 12
ADH67966
ID ADH67966 standard; peptide; 73 AA.

AC ADH67966;

DT 25-MAR-2004 (first entry)

DE Composition targeting ligand peptide Albolabrin.

KM bioactive agent; anionic lipid; cationic counter ion;

KW lipid covalently bonded to a polymer; ultrasound; charged lipid;

KM targeted drug delivery; diagnostic imaging; targeting ligand;

KW GPIIb/IIIa receptor; diagnosis; vascular thrombosis; clot.

OS Unidentified.

PN WO9842383-A1.

PD 01-OCT-1998.

PF 25-FEB-1998; 98WO-US003632.

PR 21-MAR-1997; 97US-00823791.

PR 06-MAY-1997; 97US-00851780.

PR 18-JUN-1997; 97US-00877826.

PR 02-JUL-1997; 97US-00889215.

PR 08-SEP-1997; 97US-00925353.

PA (IMAR-) IMARX PHARM CORP.

PI Unger EC;

DR WPI; 1998-557028/47.

PT Processes for drug delivery, therapeutic imaging and diagnostic imaging -
PT comprises use of compositions comprising charged lipid, counterion and
PT lipid covalently bonded to polymer.

PS Disclosure; Page 68; 167pp; English.

CC The invention relates to a method of: (A) delivering a bioactive agent
CC (BA) to a patient by: (a) administering a composition comprising: (i) an
CC anionic lipid (AL); (ii) a cationic counter ion (CCI); (iii) a lipid
CC covalently bonded to a polymer (LBP), and (iv) BA, and (b) applying
CC therapeutic ultrasound to facilitate delivery of BA in a desired region;
CC (B) delivering a BA to a patient, comprising administering a composition
CC comprising a charged lipid (CL), a counter ion (CI), LBP, BA and
CC targeting ligand (TL); (C) providing an image of an internal region of a
CC patient, comprising: (a) administering a composition comprising CL, CI
CC and LBP of the composition in (B), and (b) scanning the patient using
CC diagnostic imaging, to give visible images of the region, and (D)
CC contrast agent comprising components as in (Ca). The
CC compositions/processes described above may be used in drug delivery.
CC targeted drug delivery, therapeutic imaging and diagnostic imaging. This
CC sequence represents an example of a targeting ligand designated
CC Albolabrin.

CC Sequence 73 AA;

Db 1 EAGEBCDCCGAPANPCCDATCKLBPAGCGEGLCCDCCSFMKGTICRRAGDDLDYCN 60
 QY 61 GISAGCPNPFHA 73
 Db 61 GISAGCPNPLHA 73

RESULT 15

ABU63163
 ID ABU63163 standard; protein; 73 AA.

AC ABU63163;

DT 17-SEP-2003 (first entry)

DE Targeting ligand #13 used in novel diagnostic ultrasound method.

KW ultrasound method; targeted vesicle composition; targeting ligand;
 KW ultrasound scanning; dual frequency ultrasound insonation; micelle;
 KW liposome; phospholipid; ultrasound energy; vesicle oscillation;
 KW reflected ultrasound signal; ultrasound diagnosis; echogenic thrombus;
 KW endothelial tissue; epithelial cell; tumour cell; myocardial cell;
 KW integrin; malignancy; inflammation; heart; diseased tissue; imaging;
 KW gastrointestinal region; lymphatic system.

OS Synthetic.

PN US6521211-B1.

PD 18-FEB-2003.

PF 03-FEB-1999; 99US-00243640.

PR 07-JUN-1995; 95US-00497684.

PR 01-MAY-1996; 96US-00640464.

PR 06-JUN-1996; 96US-00660032.

PR 06-FEB-1998; 98US-0073913P.

PR 22-DEC-1998; 98US-00218660.

PA (BRIM) BRISTOL-MYERS SQUIBB MEDICAL IMAGING INC.

PI Unger EC, Wu Y;

DR WPI, 2003-S31036/50.

XX Ultrasound diagnosis, by administering targeted vesicle composition with

PT vesicles encapsulating gas, in combination with targeting ligand, to a

PT patient, and scanning patient by dual frequency ultrasound insonation.

XX Disclosure; Col 50; 96pp; English.

XX The present invention relates to a novel ultrasound method which involves

CC administering to a patient a targeted vesicle composition which comprises

CC vesicles encapsulating a gas, in combination with a targeting ligand, and

CC scanning the patient using dual frequency ultrasound insonation. The

CC vesicles themselves comprise a lipid, protein or polymer, and are

CC selected from liposomes and micelles. The vesicles may comprise a

CC phospholipid selected from dioleoylphosphatidylcholine,

CC dimyristoylphosphatidylcholine, dipalmitoylphosphatidylcholine,

CC distearoylphosphatidylcholine, dipalmitoylphosphatidylethanolamine,

CC succinylidistearoylphosphatidylethanolamine, N-

CC palmitoyldioleoylphosphatidylethanolamine and phosphatidic acids. The method of

CC scanning involves exposing the patient to a first ultrasound energy,

CC and then subsequently, while the vesicle is oscillating, exposing the

CC patient to a second ultrasound energy having a second insonation

CC frequency that is different from the first insonation frequency, and

CC detecting the reflected ultrasound signal. The method is useful for

CC ultrasound diagnosis, for detection of a thrombus or enhancement of

CC thrombus (e.g. old or echogenic thrombus) and for detecting vesicles

CC endothelial tissue including integrins associated with malignancy or
 CC inflammation. The method is also useful for diagnosing the presence or
 CC absence of diseased tissue in a patient and for imaging one or more
 CC regions of a patient, such as for providing images of the heart,
 CC gastrointestinal region or lymphatic systems. ABU63151-ABU63172 represent
 CC targeting ligands that may be used in the method of the present invention
 XX

SO Sequence 73 AA;

Query Match 90.3%; Score 391; DB 7; Length 73;
 Best Local Similarity 87.7%; Pred. No. 5.6e-28;
 Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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 Db 1 EAGEBCDCCGAPANPCCDATCKLBPAGCGEGLCCDCCSFMKGTICRRAGDDLDYCN 60
 QY 61 GISAGCPNPFHA 73
 Db 61 GISAGCPNPLHA 73

Search completed: December 3, 2004, 21:35:44
 Job time : 117 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 18:04:21 / Search time 408 Seconds
(without alignments)
2740.507 Million cell updates/sec

Title: US-10-089-473a-2
Perfect score: 213
Sequence: 1 ggaagaagaatgcagctgtg.....ccagaatccctccatgc 213

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4134886 segs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
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3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002as:*
7: Geneseq2002bs:*
8: Geneseq2003as:*
9: Geneseq2003bs:*
10: Geneseq2003cs:*
11: Geneseq2003ds:*
12: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	213	100.0	213	6	AAD31060
2	213	100.0	222	8	ACC44733
3	198.6	93.2	1558	2	AAQ50394
4	197	92.5	222	3	AAZ55609
5	190.6	89.5	2029	5	AAZ94881
6	190.6	89.5	2029	5	AAD07386
7	185.8	87.2	2102	6	ABS54623
8	174.6	82.0	222	8	ACC47594
9	154.8	72.7	174	2	AAQ50357
10	153.2	71.9	174	2	AAQ44933
11	153.2	71.9	174	2	AAQ50385
12	151.6	71.2	174	2	AAQ44932
13	151.6	71.2	174	2	AAQ50390
14	151.6	71.2	174	2	AAQ50384
15	150	70.4	174	2	AAQ44934
16	150	70.4	174	2	AAQ50386
17	150	70.4	174	2	AAQ44939
18	150	70.4	174	2	AAQ44940
19	150	70.4	174	2	AAQ44938
20	150	70.4	174	2	AAQ50393
21	150	70.4	174	2	AAQ44941

22	150	70.4	174	2	AAQ50391	Aag50391 Platelet
23	150	70.4	174	2	AAQ50392	Aag50392 Platelet
24	148.4	69.7	174	2	AAQ44936	Aag44936 pAgalpnas
25	148.4	69.7	174	2	AAQ50387	Aag50387 Platelet
26	148.4	69.7	174	2	AAQ44935	Aag44935 pAgalpnas
27	148.4	69.7	174	2	AAQ44937	Aag44937 Platelet
28	148.4	69.7	174	2	AAQ50388	Aag50388 Platelet
29	148.4	69.7	174	2	AAQ50389	Aag50389 Platelet
30	144.6	67.9	598	6	ABK10642	Abk10642 Cottoconou
31	143	67.1	908	6	ABK10648	Abk10648 Cottoconou
32	135.4	63.6	1434	6	ABS54624	ABS54624 Disintegr
33	125.8	59.1	226	2	AAQ05730	AaQ05730 Platelet
34	124.2	58.3	1213	6	ABK10638	Abk10638 Pigmy rat
35	122.6	57.6	2334	6	ABK10644	Abk10644 Pigmy rat
36	122.4	57.5	229	2	AAQ10160	AaQ10160 Trigramin
37	120	56.3	288	2	AAQ25315	AaQ25315 Encodes b
38	119.6	56.2	288	2	AAQ25314	AaQ25314 Encodes b
39	111.4	52.3	1851	5	AAQ85063	AaQ85063 E. carina
40	111.4	52.3	1863	8	ABK93715	Abk93715 Human chr
41	111.4	52.3	1863	8	ABK93010	Abk93010 Saw-scale
42	106.4	50.0	333	6	ABK10649	Abk10649 Cottoconou
43	106.4	50.0	585	6	ABK10643	Abk10643 Cottoconou
44	101.2	47.5	2240	6	ABK14952	Abk14952 Korean ad
45	100.8	47.3	226	2	ADP66009	ADP66009 Snake ven

ALIGNMENTS

RESULT 1	
AAQ31060	
ID	AAQ31060 standard; cDNA; 213 bp.
XX	
AC	AAQ31060;
XX	
DT	29-AUG-2003 (revised)
DT	07-AUG-2003 (revised)
DT	18-JUN-2002 (first entry)
XX	
DE	Agkistrodon saxatilis emelianov saxatillin cDNA.
XX	
XX	Korean snake; saxatillin; anticoagulant; cytostatic; venom; anti-tumour;
KM	platelet aggregation; angiogenesis; cytotoxicity; ss.
XX	
OS	Glycydus halys.
XX	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	1..213
FT	/*tag= "a
FT	/product= "saxatillin protein"
FT	/transl_except= (pos:1..3, aa:Glu-Ala-Gly)
FT	/note= "Deletion of 6 bases alters the reading frame; CDS
FT	does not include start and stop codon"
FT	/partial
XX	
PD	WO200214488-A1.
XX	
PF	21-FEB-2002.
XX	
PR	26-JUL-2000; 2000WO-KR000809.
XX	
PR	26-JUL-2000; 2000WO-KR000809.
XX	
PA	(CHUN/) CHUNG K.
PA	(KIMD/) KIM D.
XX	
PI	Hong S, Koh Y, Sohn Y, You W, Jang Y, Huh C;
XX	
DR	WPI; 2002-241903/29.
XX	
DR	P-PSDB; AAB19787.
XX	
PT	New cDNA encoding Saxatillin protein derived from venom of Korean snake
PT	Agkistrodon saxatilis emelianov; useful as anti-platelet aggregation

PT agent and anti-tumor agent.
XX
PS Claim 1, Page 36; 41pp; English.
XX
CC The invention relates to a cDNA encoding Saxatillin protein derived from
CC venom of Korean snake Agkistrodon saxatilis emelianov. The cDNA is useful
CC for as an anti-tumor agent and for effectively suppressing platelet
CC aggregation which makes it possible as an active ingredient of anti-
CC platelet agent. Saxatillin is useful for inhibiting angiogenesis induced
CC by tumor and for inhibiting tumor without cytotoxicity. The present
CC sequence is Agkistrodon saxatilis emelianov saxatillin cDNA. (Updated on
CC 07-AUG-2003 to correct OS field.) (Updated on 29-AUG-2003 to standardise
CC OS field)
XX
SQ Sequence 213 BP; 56 A; 45 C; 65 G; 47 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 213; DB 6; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.5e-62;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAGAGAAATGTGACTGTGGCGCTCTCTGCAATCCGTCTGCGATGCTGCAACCTGTAAA 60
DB 1 GGAGAGAAATGTGACTGTGGCGCTCTCTGCAATCCGTCTGCGATGCTGCAACCTGTAAA 60
QY 61 CTGAGACCAAGGGCGCGAGTGTGCAAGAGACTGTGTGTGACCACTGCAATTATGAAA 120
DB 61 CTGAGACCAAGGGCGCGAGTGTGCAAGAGACTGTGTGTGACCACTGCAATTATGAAA 120
QY 121 GAAGAACATATATGCCGATGCGCAAGGGGTGATGATGATTAATGCAATGGCATA 180
DB 121 GAAGAACATATATGCCGATGCGCAAGGGGTGATGATGATTAATGCAATGGCATA 180
QY 181 TCTGCTGCTGTCTGCCAGAAATCCCTTCATGCC 213
DB 181 TCTGCTGCTGTCTGCCAGAAATCCCTTCATGCC 213
XX
RESULT 2
ACCA4733
ID ACCA4733 standard; cDNA; 222 BP.
XX
AC ACCA4733;
XX
DT 27-OCT-2003 (revised)
DT 29-MAY-2003 (first entry)
XX
DE Agkistrodon saxatilis saxatillin cDNA sequence SEQ ID NO:1.
XX
KW Agkistrodon saxatilis; saxatillin; anti-cancer; cancer; disintegrin;
KW tumor; lipoplex; cancer growth inhibition; cationic liposome;
KW cytosolic; gene therapy; gene; ss.
XX
OS Gloydius halye.
XX
FN WO2003018065-A1.
XX
PD 06-MAR-2003.
XX
PF 29-AUG-2001; 2001WO-KR001461.
XX
PR 29-AUG-2001; 2001WO-KR001461.
XX
PA (CHUN/) CHUNG K.
XX
PI Chung K, Park Y, Kim S, Hong S, Sohn Y, Jang Y, Hun C, Kim D;
XX
DR MPI; 2003-278621/27.
XX
PT Lipoplex useful for inhibiting growth of cancer cells, and for treating
PT or preventing cancer, comprises a cationic liposome and an expression
PT vector containing the saxatillin gene.
XX
PS Claim 1, Page 20; 24pp; English.

XX
CC The present invention describes a lipoplex for inhibiting cancer growth
CC comprising a cationic liposome and an expression vector containing a
CC saxatillin gene having a sequence of 222 base pairs (bp), given in
CC ACCA4733. Also described is a method for inhibiting cancer growth by
CC using a saxatillin gene, which comprises: (a) mixing cholesterol with
CC DOPAC, suspending the mixture in aqueous medium to prepare cationic
CC liposome, and introducing saxatillin gene to eukaryotic vector; (b) mixing
CC the cationic liposome and expression vector in aqueous medium and
CC homogenizing to prepare lipoplex; and (c) introducing the lipoplex to a
CC cancer tissue. Saxatillin is a disintegrin gene which has cytostatic
CC activity and can be used in gene therapy. The lipoplex is useful for
CC inhibiting growth of cancer cells, and for treating or preventing cancer.
CC (Updated on 27-Oct-2003 to standardise OS field)
XX
SQ Sequence 222 BP; 59 A; 47 C; 68 G; 48 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 213; DB 8; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.5e-62;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAGAGAAATGTGACTGTGGCGCTCTCTGCAATCCGTCTGCGATGCTGCAACCTGTAAA 60
DB 7 GGAGAGAAATGTGACTGTGGCGCTCTCTGCAATCCGTCTGCGATGCTGCAACCTGTAAA 66
QY 61 CTGAGACCAAGGGCGCGAGTGTGCAAGAGACTGTGTGTGACCACTGCAATTATGAAA 120
DB 67 CTGAGACCAAGGGCGCGAGTGTGCAAGAGACTGTGTGTGACCACTGCAATTATGAAA 126
QY 121 GAAGAACATATATGCCGATGCGCAAGGGGTGATGATGATTAATGCAATGGCATA 180
DB 127 GAAGAACATATATGCCGATGCGCAAGGGGTGATGATGATTAATGCAATGGCATA 186
QY 181 TCTGCTGCTGTCTGCCAGAAATCCCTTCATGCC 213
DB 187 TCTGCTGCTGTCTGCCAGAAATCCCTTCATGCC 219
XX
RESULT 3
AAO50394
ID AAO50394 standard; cDNA to mRNA; 1558 BP.
XX
AC AAO50394;
XX
DT 24-OCT-2003 (revised)
DT 11-MAY-1994 (first entry)
XX
DE Platelet aggregation inhibitory peptide.
XX
KW Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF; ss.
XX
OS Gloydius halye blomhoffi.
XX
FN Key Location/Qualifiers
FT CDS 10..1452
FT /tag= a
XX
PN JP05255395-A.
XX
PD 05-OCT-1993.
XX
PF 03-OCT-1991; 91JP-00256234.
XX
PR 26-OCT-1990; 90JP-00287116.
PR 20-FEB-1991; 91JP-00026328.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
DR WPI; 1993-348481/44.
DR P-PSTB; AAR42867.
XX
PT Polypeptide of specified aminoacid sequence - used for inhibiting
PT platelet aggregation caused by e.g. collagen, thrombin, etc.

```
XX Example; Page 33-35; 50pp; Japanese.
XX
XX The sequence is that encoding a polypeptide which inhibits platelet
CC aggregation caused by ADP, collagen, thrombin, arachidonic acid and PAF.
CC (Updated on 24-OCT-2003 to standardise OS field)
CC
XX Sequence 1558 BP; 468 A; 310 C; 362 G; 418 T; 0 U; 0 Other;
SO
Query Match          93.2%; Score 198.6; DB 2; Length 1558;
Best Local Similarity 95.8%; Pred. No. 3e-57;
Matches 204; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GGAGAGAATGTGACTGTGGGCTCTGCAAAATCCGTGTGCGATGCTGCACCTGTAA 60
Db 1237 GGAGAAGAGTGTGACTGTGGCTCTCGGAAATCCGTGTGCGATGCTGCACCTGTAA 1296
QY 61 CTGAGACCGAGGGCGCGAGTGTGCAGAGACTGTGTGTGACCACTGCAGATTATGAAA 120
Db 1297 CTGAGACAGGGGGCGACAGTGTGCAGAGACTGTGTGTGACCACTGCAGATTATGAAA 1356
QY 121 GAAGAACAAATATCCCGATGCGAAGGGGTGATGACATGATGATTACTGCAATGGCAT 180
Db 1357 AAAAGAACAGTATCCCGATGCGAAGGGGTGATGACATGATGATTACTGCAATGGCAT 1416
QY 181 TCTGCTGGCTGTCCAGAAATCCCTTCATGCC 213
Db 1417 TCTGCTGGCTGTCCAGAAATCCCTTCATGCC 1449
RESULT 4
AAZ55609
ID AAZ55609 standard; cDNA; 222 BP.
XX
AC AAZ55609;
XX
DT 15-SEP-2003 (revised)
DT 27-MAR-2000 (first entry)
XX
DE Korean snake venom salmosin cDNA.
XX
KW Salmosin; angiogenesis; inhibitor; integrin; antagonist; disintegrin;
KW metastasis; cancer; tumour; ss.
XX
OS Gloydius halys.
XX
FH Key Location/Qualifiers
FT mat_peptide 1..219
FT /*tag= a
FT /product= "Korean snake salmosin"
XX
XX EP967276-A2.
XX
XX 29-DEC-1999.
XX
XX 23-JUN-1999; 99EP-00304935.
XX
XX 23-JUN-1998; 98KR-00023778.
XX 04-JUN-1999; 99KR-00020579.
XX
XX (KIMD/) KIM D.
XX
XX Kim D, Chung KH, Kang I;
XX
XX WPI, 2000-064611/06.
XX P-PSDB; AAY58231.
XX
XX Novel polypeptides used for antitumor therapy.
XX
XX Claim 7; Page 14; 24pp; English.
XX
XX This sequence represents cDNA encoding the 7.5 kD salmosin protein of a
XX Korean snake, Agkistrodon halys brevicaudus. Salmosin is a disintegrin, a
```

```
CC family of small proteins mainly derived from snake venom which contain an
CC RGD or KGD motif (the structural motif recognised by platelet fibrinogen
CC receptor alpha-2-b-beta-3). Disintegrins act as potent antagonists of
CC several integrins including alpha-v-beta-3 and alpha-5-beta-1 integrins,
CC the former being a marker of angiogenic blood vessels and certain
CC malignant cells. Disintegrins inhibit tumour metastasis by blocking
CC tumour cell adhesion to the extracellular matrix, and antagonism of
CC integrin alpha-v-beta-3 can suppress tumour-induced angiogenesis.
CC Salmosin can be used as an anticancer agent. It may be used for the
CC inhibition or reduction of tumour cell angiogenesis, the inhibition of
CC metastatic tumour formation and the inhibition or reduction of metastatic
CC tumour growth. Nucleotides encoding salmosin may be used in gene therapy
CC applications. Many types of cancer may be treated with salmosin or
CC nucleotides encoding it, including leukaemia and cancers of the breast,
CC ovary, uterus, skin, lung, larynx, colon, pancreas, testis, liver, brain,
CC muscle and bone. (Updated on 15-SEP-2003 to standardise OS field)
XX
XX Sequence 222 BP; 62 A; 46 C; 66 G; 48 T; 0 U; 0 Other;
SQ
Query Match          92.5%; Score 197; DB 3; Length 222;
Best Local Similarity 95.3%; Pred. No. 4.7e-57;
Matches 203; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 GGAGAGAATGTGACTGTGGGCTCTCTGCAAAATCCGTGTGCGATGCTGCACCTGTAA 60
Db 7 GGAGAGAATGTGACTGTGGCTCTCTGCAAAATCCGTGTGCGATGCTGCACCTGTAA 66
QY 61 CTGAGACCGAGGGCGCGAGTGTGCAGAGACTGTGTGTGACCACTGCAGATTATGAAA 120
Db 67 CTGAGACAGAGGACACAGTGTGCAGAGACTGTGTGTGACCACTGCAGATTATGAAA 126
QY 121 GAAGAACAAATATCCCGATGCGAAGGGGTGATGACATGATGATTACTGCAATGGCAT 180
Db 127 GAAGAACAAATATCCCGATGCGAAGGGGTGATGACATGATGATTACTGCAATGGCAT 186
QY 181 TCTGCTGGCTGTCCAGAAATCCCTTCATGCC 213
Db 187 TCTGCTGGCTGTCCAGAAATCCCTTCATGCC 219
RESULT 5
AAZ94881
ID AAZ94881 standard; cDNA; 2029 BP.
XX
AC AAZ94881;
XX
DT 01-AUG-2000 (first entry)
DT
XX
DE Southern copperhead snake conortrostatin cDNA.
XX
KW Southern copperhead snake; venom; conortrostatin; disintegrin;
KW cytostatic; antiproliferative; thrombolytic; cerebroprotective;
KW antitumor; antiarteriosclerotic; antiangiogenic; cardiatic; metastasis;
KW thrombolysis; thromboembolism; stroke; arteriosclerosis; atherosclerosis;
KW embolism; aneurism; angina; myocardial infarction; integrin; ss.
XX
XX Agkistrodon conortroix.
XX
OS
XX
FH Key Location/Qualifiers
FT CDS 87..1538
FT /*tag= a
FT /transl_except= (pos:1023..1025, aa:Ala)
FT polyA_signal 1988..1993
FT /*tag= b
FT polyA_site 2010..2020
FT /*tag= c
XX
XX WC0200018421-A1.
XX
XX 06-APR-2000.
XX
XX 29-SEP-1999; 99WO-US022608.
```

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PR 29-SEP-1998; 98US-00163047.
XX (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
XX Markland FS, Zhou Q;
XX
XX WPI; 2000-303389/26.
XX P-PSDB; AAY79413.
XX
XX Novel proteins and polynucleotides representing conortrostatin useful
XX for inhibiting platelet aggregation, tumor metastasis and growth.
XX
XX Claim 9; Fig 3A-D; 8app; English.
XX
XX The present sequence is that of claimed DNA encoding the Southern
XX copperhead snake venom disintegrin, conortrostatin (see AAY79413), a
XX protein that inhibits the interactions between integrins and their
XX receptors. The DNA was obtained from a venom gland cDNA library by PCR
XX amplification using primers (see AAY79413-83) based on a conserved region
XX of disintegrins. Conortrostatin precursor protein includes a pro-protein
XX region, a metalloproteinase region which includes a metal-binding motif,
XX and a disintegrin region which includes an RGD loop that acts as an
XX integrin antagonist. DNA molecules consisting of nucleotides 1341-1535
XX (encoding the disintegrin), 657-1316 (metalloproteinase), 87-656 (pro-
XX protein) and 87-1535 (entire precursor protein) of the present sequence
XX are also claimed. These can be used in the recombinant production of
XX conortrostatin proteins. The purified proteins are used in
XX pharmaceutical compositions for treating diseases associated with an
XX integrin binding to an integrin receptor, especially to inhibit platelet
XX aggregation, tumor metastasis, angiogenesis, neovascularization, cell
XX adhesion, invasiveness, or growth (all claimed). The proteins are also
XX useful for treating a thrombotic disorder, e.g. preventing arterial,
XX venous, and microvascular thrombosis and thromboembolism, stroke,
XX transient ischaemic attacks, arteriosclerosis, atherosclerosis, pulmonary
XX embolism, aneurysm, angina and myocardial infarction
XX
XX Sequence 2029 BP; 630 A; 433 C; 423 G; 543 T; 0 U; 0 Other;
SQ
Query Match 89.5%; Score 190.6; DB 3; Length 2029;
Best Local Similarity 93.4%; Pred. No. 1.8e-54;
Matches 199; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 GGAGAAAGATGTGACTGTGGCGCTCTGCAAAATCCGTCTCGATGTCGAACCTGTAAA 60
DB 1323 GGAGAAAGAAAGTGAATTGACGCTCTGCAAAATCCGTCTCGATGTCGAACATGTAAA 1382
QY 61 CTGAGACCAAGGGCGCCAGTGTGCAAGAGACTGTGTGTGACCAAGTCAAGATTATGAAA 120
DB 1383 CTGACAAACAGGGTCAAGTGTGCAAGTGTGTGTGACCAAGTCAAGATTATGAAA 1442
QY 121 GAAGAACAAATATGCCCGATGCAAGGGGTATGATGATGATTAATGCAATGGCATA 180
DB 1443 GAAGAACAGTATGCGGAGAGAGCAAGGGGTATGATGATGATTAATGCAATGGCATA 1502
QY 181 TCTGTGGCTGTCCCAAGAAATCCCTTCATGCC 213
DB 1503 TCTGTGGCTGTCCCAAGAAATCCCTTCATGCC 1535

```

```

KW wound healing; ss.
XX
XX Agkistrodon conortrix.
XX
XX Key Location/Qualifiers
XX 5'UTR 1..86
XX /tag= a
XX /tag= b
XX /tag= c
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QY 181 TCTGCTGCTGTCCAGAAATCCCTTCATGCC 213
DB 1503 TCTGCTGCTGTCCAGAAATCCCTTCATGCC 1535

RESULT 7
AB554623
ID AB554623 standard; cDNA; 2102 BP.
AC AB554623;
XX
XX 28-NOV-2002 (first entry)
DE Disintegrin protease ZSNK16 cDNA.
XX
XX ss; gene; ZSNK16; disintegrin protease; antifertility; vulnery;
KW anticoagulant; thrombolytic; cell-matrix; cell-cell interaction;
KW cell proliferation; cell differentiation; immune recognition;
KW fertilisation; growth control; angiogenesis; fertility; tumour;
KW gamete maturation; immunology; coagulation; thrombosis; trauma;
KW epithelial disorder.
XX
XX Sistrurus miliarius.
OS
XX
XX Key Location/Qualifiers
FT CDS 88..1524
FT /*tag= a
FT /product= "ZSNK16"
FT sig_peptide 88..141
FT /*tag= b
FT misc_feature 142..648
FT /*tag= c
FT /note= "Encodes propeptide"
FT mat_peptide 649..1521
FT /*tag= d
FT /label= Mature_ZSNK16
XX
XX MO200268458-A2.
XX
XX 06-SEP-2002.
XX
XX 20-FEB-2002; 2002WO-US004937.
XX
XX 20-FEB-2001; 2001US-0270276P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Fox B, Shepard PO;
XX
XX WPI; 2002-706967/76.
DR P-PSDB; ABG70857.
XX
XX
XX New disintegrin protease (designated ZSNK16) homolog polypeptides, useful
PT in modulating cell-cell interactions, delivering therapeutic agents, or
PT as replacement therapy for e.g. fertility, coagulation, thrombosis or
PT trauma.
XX
XX
XX Disclosure; Page 70-73; 77pp; English.
XX
XX The invention relates to a new isolated polypeptide, which is a
CC disintegrin protease designated ZSNK16 from Sistrurus miliarius,
CC comprising an integrin binding region (designated ZSNK16-1br) or a zinc-
CC binding motif (designated ZSNK16-zbm). Also included are the nucleic acid
CC encoding ZSNK16, a ZSNK16 expression vector a transformed cultured cell
CC expressing ZSNK16, producing anti-ZSNK16 antibodies, and a nucleic acid
CC encoding fusion proteins of the ZSNK16-1br and ZSNK16-zbm domains. The
CC polypeptide is useful as a tool for investigating cell-matrix and cell-
CC cell interactions, for studying cell proliferation or differentiation in
CC human tissues, for studying immune recognition, fertilisation, growth
CC control or angiogenesis, for identifying inhibitors of its activity, or
CC for delivering therapeutic agents (e.g. proteases, radionuclides,
CC chemotherapy agents or small molecules). The ZSNK16 polypeptide is also
CC useful as replacement therapy for disorders associated with cell-cell

CC interactions, e.g. fertility, gamete maturation, immunology, coagulation,
CC thrombosis, trauma or epithelial disorders. The polypeptide is also
CC useful in the development of antithrombotic and antineoplastic agents due
CC to their anti-adhesive, anti-migration of certain tumour cells, and anti-
CC angiogenesis activities. The antibodies to the ZSNK16 polypeptide are
CC useful for tagging cells that express ZSNK16, for isolating ZSNK16 by
CC affinity purification, for detecting or quantifying soluble ZSNK16 as
CC marker of underlying pathology or disease, or for screening expression
CC libraries. The present sequence encodes ZSNK16
XX
XX Sequence 2102 BP; 656 A; 431 C; 442 G; 573 T; 0 U; 0 Other;
SQ
Query Match 87.2%; Score 185.8; DB 6; Length 2102;
Best Local Similarity 92.0%; Pred.No. 8.1e-53;
Matches 196; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1 GGAGAAATGTGACTGTGGCGCTCCTGCAATCCGTGTGGATGCAACCTGTAA 60
DB 1309 GGAGAAATGTGACTGTGGCGCTCCTGCAATCCGTGTGGATGCAACCTGTAA 1368
QY 61 CTGAGACAGGGGCGCAGTGTGCAGAGACTGTGTGACCACTGCAGATTATGAA 120
DB 1369 CTGAGACAGGGGCGCAGTGTGCAGAGACTGTGTGACCACTGCAGATTATGAA 1428
QY 121 GAAGAACATATGCCGATGGCAAGGGGTATGACATGAGATGATTACTGCATATGGCATA 180
DB 1429 AAGAGAAATATGCGCGAGACCAAGGGGTATGACCGGATGATGCTGACGACCA 1488
QY 181 TCTGCTGCTGTCCAGAAATCCCTTCATGCC 213
DB 1489 TCTGCTGCTGTCCAGAAATGCTTCATGCC 1521

RESULT 8
ACCA47594
ID ACCA47594 standard; cDNA; 222 BP.
XX
XX ACCA47594;
XX
XX 23-JUN-2003 (first entry)
XX
XX Disintegrin-gamma cDNA, SEQ ID NO:3.
XX
XX Disintegrin-gamma; cysteine-rich; RGD motif; integrin antagonist;
KW inhibition; vascularisation; tumour growth; tumour metastasis; cancer;
KW cytostatic; gene; ss.
XX
XX Unidentified.
OS
XX
XX
XX Key Location/Qualifiers
FH CDS 1..222
FT /*tag= a
FT /partial
FT /product= "Disintegrin-gamma"
FT /note= "No start codon given in the specification"
FT /transl_except= (pos:16..18, aa:Tyr)
FT /transl_except= (pos:46..48, aa:Tyr)
FT /transl_except= (pos:124..126, aa:Gln)
FT /transl_except= (pos:127..129, aa:Gln)
FT /note= "The above translation exceptions relate only to
the version of disintegrin-gamma shown in ABP97447)"
XX
XX CN1374318-A.
XX
XX 16-OCT-2002.
XX
XX 08-FEB-2002; 2002CN-00103679.
XX
XX 08-FEB-2002; 2002CN-00103679.
XX
XX (MIUJ/) MI J.
XX
XX M4 J;
PI

```
XX WPI; 2003-168400/17.
DR P-PDSB; ABP97447, ABP97448.
XX
XX New natural dissociation essence gamma gene and antineoplastic active
PT polypeptide dissociation essence-gamma, useful as a fusion body
PT antagonist to inhibit vascularization, tumor metastasis and tumor growth.
XX
XX Claim 1; Page 7 (Disclosure); 12pp; Chinese.
XX
XX The invention relates to a disintegrin-gamma protein (ABP97447, ABP97448)
CC and nucleic acids encoding it (ACC47594). Disintegrin-gamma is cysteine-
CC rich, contains an RGD integrin-binding motif, and acts as an integrin
CC antagonist. Disintegrin gamma may be used to inhibit integrin-mediated
CC activities such as vascularization, and tumor growth and metastasis. The
CC present sequence represents cDNA encoding disintegrin-gamma
XX
SQ Sequence 222 BP; 67 A; 49 C; 62 G; 44 T; 0 U; 0 Other;
Query Match 82.0%; Score 174.6; DB 8; Length 222;
Best Local Similarity 88.7%; Pred. No. 2.2e-49;
Matches 189; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 1 GGAGAAAGATGTGACTGTGGCGCTCTGCAAAATCCGTCCTGCAACTGTGAAA 60
DB 7 GGAAGAAAGATGTGACCGGAGCTCTTGTGCAAAATCCGTCGATGCTGCAAACTGTAAA 66
QY 61 CTGAGACCAAGGCGCGCAGTGTGACAGAAAGACTGTGTGTGACAGTCAGATTATGAAA 120
DB 67 CTGAACCAAGAGACGACGATGTACAGAGACCGCTGTGTGTGACAGGCGAATTTAAAGAA 126
QY 121 GAAGAACATATATGCGGATGCGCAAGGGGTGATGATGATGATTACTGCAATGCGATA 180
DB 127 GAAGAACATATATGCGGATGCGCAAGGGGTGATGATGATGATTACTGCAATGCGATA 186
QY 181 TCTGCTGCTGTCCGAGAAATCCCTCCATGCGC 213
DB 187 TCTGCTGCTGTCCGAGAAATCCCTCCATGCGC 219
RESULT 9
AAQ50357
ID AAQ50357 standard; cDNA; 174 BP.
XX
XX AAQ50357;
AC 24-OCT-2003 (revised)
DT 11-MAY-1994 (first entry)
XX
DE pAgalphi201 platelet aggregation inhibitory polypeptide.
XX
XX Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF; ss.
XX
XX Gloydins hays biomoffi.
XX
XX JP05255395-A.
XX
XX 05-OCT-1993.
XX
XX 03-OCT-1991; 91JP-00256234.
XX
XX 26-OCT-1990; 90JP-00287116.
XX
XX 20-FEB-1991; 91JP-00026328.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX WPI; 1993-348481/44.
XX
XX P-PDSB; AAR42887.
XX
XX Polypeptide of specified aminoacid sequence - used for inhibiting
XX platelet aggregation caused by e.g. collagen, thrombin, etc.
PS Example; Fig 3; 50pp; Japanese.
```

```
XX The sequence is that of pAgalphi201 cDNA which comprises a polypeptide
CC isolated from Agkistrodon hays biomoffi. It was used in the isolation
CC and prodn. of a polypeptide inhibiting platelet aggregation caused by
CC ADP, collagen, thrombin, arachidonic acid and PAF. (Updated on 24-OCT-
XX 2003 to standardise OS field)
XX
SQ Sequence 174 BP; 50 A; 31 C; 55 G; 38 T; 0 U; 0 Other;
Query Match 72.7%; Score 154.8; DB 2; Length 174;
Best Local Similarity 93.1%; Pred. No. 1.2e-42;
Matches 162; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 4 GAGAGATGTGACTGTGGCGCTCTGCAAAATCCGTCCTGCAACTGTGAAAAC 63
DB 1 GAGAGCTGCACTGTGGCTCTCTCTGCAAAATCCGTCCTGATGCTGCAACTGTAAAAC 60
QY 64 AGACCAAGGCGCGCAGTGTGACAGAAAGACTGTGTGTGACAGTCAGATTATGAAAAG 123
DB 61 AGACCAAGGCGCAGTGTGACAGAAAGACTGTGTGTGACAGTCAGATTATGAAAAG 120
QY 124 GAAGAACATATGCGGATGCGCAAGGGGTGATGATGATGATTACTGCAATGCG 177
DB 121 GGAACAGTATGCCCGATAGCAAGGGGTGATGATGATGATTACTGCAATGCG 174
RESULT 10
AAQ44933
ID AAQ44933 standard; cDNA; 174 BP.
XX
XX AAQ44933;
AC 24-OCT-2003 (revised)
DT 11-MAY-1994 (first entry)
XX
DE pAgalphi2-101 platelet aggregation inhibitory polypeptide.
XX
XX Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF; ss.
XX
XX Gloydins hays biomoffi.
XX
XX JP05255395-A.
XX
XX 05-OCT-1993.
XX
XX 03-OCT-1991; 91JP-00256234.
XX
XX 26-OCT-1990; 90JP-00287116.
XX
XX 20-FEB-1991; 91JP-00026328.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX WPI; 1993-348481/44.
XX
XX P-PDSB; AAR46947.
XX
XX Polypeptide of specified aminoacid sequence - used for inhibiting
XX platelet aggregation caused by e.g. collagen, thrombin, etc.
XX
XX Example; Fig 13; 50pp; Japanese.
XX
XX The sequence is that of pAgalphi2-101 cDNA which comprises a polypeptide
CC isolated from Agkistrodon hays biomoffi. It was used in the isolation
CC and prodn. of a polypeptide inhibiting platelet aggregation caused by
CC ADP, collagen, thrombin, arachidonic acid and PAF. (Updated on 24-OCT-
XX 2003 to standardise OS field)
XX
SQ Sequence 174 BP; 51 A; 31 C; 55 G; 37 T; 0 U; 0 Other;
Query Match 71.9%; Score 153.2; DB 2; Length 174;
Best Local Similarity 92.5%; Pred. No. 4.2e-42;
Matches 161; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 4 GAAGATGTGACTGTGGCGCTCTGCAAAATCCGTCCTGCAACTGTGAAAAC 63
```

Db 1 GAGGACTGCGACTGTGCTCTCCGTGAAATCCGCTGTGATGCTGCACTGTAACCTG 60
QY 64 AGACCAAGGGGGCGGCTGTGCAAGAGACTGTGTGTACCAAGTGCAGATTATGAAGAA 123
Db 61 AGACCAAGGAGACAGTGTGTGCAAGAGACTGTGTGTGTACCAAGTGTGCAATTATGAAGAAAA 120
QY 124 GGAACAAATATGCCGATGCGCAAGGGGTGATGACATGATGATTACTGCAATGGC 177
Db 121 GGAACAGTATGCCGATAGCAAGGGGTGATGACATGATGATTACTGCAATGGC 174

RESULT 11

AAQ50385
ID AAQ50385 standard; cDNA to mRNA; 174 BP.

AC AAQ50385;

DT 24-OCT-2003 (revised)
DT 11-MAY-1994 (first entry)

DE Platelet aggregation inhibitory peptide.

KW Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF; ss.

OS Gloydius halys blomhoffi.

PN JP05255395-A.

PD 05-OCT-1993.

PF 03-OCT-1991; 91JP-00256234.

PR 26-OCT-1990; 90JP-00287116.

PR 20-FEB-1991; 91JP-00026328.

PA (TAKE) TAKEDA CHEM IND LTD.

DR WPI; 1993-348481/44.

DR P-PSDB; AAR42858.

PT Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc.

PS Example; Page 27; 50pp; Japanese.

CC The sequence is that encoding a polypeptide which inhibits platelet aggregation caused by ADP, collagen, thrombin, arachidonic acid and PAF.

CC (Updated on 24-OCT-2003 to standardise OS field)

XX Sequence 174 BP; 51 A; 31 C; 55 G; 37 T; 0 U; 0 Other;

Query Match 71.9%; Score 153.2; DB 2; Length 174;

Best Local Similarity 92.5%; Pred. No. 4.2e-42; Mismatches 13; Indels 0; Gaps 0;

Matches 161; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 4 GGAAGATGCTGCTGCGCTCTGCAAAATCCGCTGCTGCAATGCTGCACTGTAACCTG 63

Db 1 GAGGACTGCGACTGTGCTCTCCGTGAAATCCGCTGTGATGCTGCACTGTAACCTG 60

QY 64 AGACCAAGGGGGCGGCTGTGCAAGAGACTGTGTGTACCAAGTGCAGATTATGAAGAA 123

Db 61 AGACCAAGGAGACAGTGTGTGCAAGAGACTGTGTGTGTACCAAGTGTGCAATTATGAAGAAAA 120

QY 124 GGAACAAATATGCCGATGCGCAAGGGGTGATGACATGATGATTACTGCAATGGC 177

Db 121 GGAACAGTATGCCGATAGCAAGGGGTGATGACATGATGATTACTGCAATGGC 174

RESULT 12
AAQ44932
ID AAQ44932 standard; cDNA; 174 BP.

AC AAQ44932;
XX 24-OCT-2003 (revised)
DT 11-MAY-1994 (first entry)
DE pAgalphi-101 platelet aggregation inhibitory polypeptide.
XX
KW Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF; ss.
OS Gloydius halys blomhoffi.

PN JP05255395-A.

PD 05-OCT-1993.

PF 03-OCT-1991; 91JP-00256234.

PR 26-OCT-1990; 90JP-00287116.

PR 20-FEB-1991; 91JP-00026328.

PA (TAKE) TAKEDA CHEM IND LTD.

DR WPI; 1993-348481/44.

DR P-PSDB; AAR46946.

PT Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc.

PS Example; Fig 12; 50pp; Japanese.

CC The sequence is that of pAgalphi-101 cDNA which comprises a polypeptide isolated from Agkistrodon halys blomhoffi. It was used in the isolation and prodn. of a polypeptide inhibiting platelet aggregation caused by

CC ADP, collagen, thrombin, arachidonic acid and PAF. (Updated on 24-OCT-2003 to standardise OS field)

XX Sequence 174 BP; 50 A; 31 C; 54 G; 39 T; 0 U; 0 Other;

Query Match 71.2%; Score 151.6; DB 2; Length 174;

Best Local Similarity 92.0%; Pred. No. 1.5e-41; Mismatches 14; Indels 0; Gaps 0;

Matches 160; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 4 GGAAGATGCTGCTGCGCTCTGCAAAATCCGCTGCTGCAATGCTGCACTGTAACCTG 63

Db 1 GAGGACTGCGACTGTGCTCTCCGTGAAATCCGCTGTGATGCTGCACTGTAACCTG 60

QY 64 AGACCAAGGGGGCGGCTGTGCAAGAGACTGTGTGTACCAAGTGCAGATTATGAAGAA 123

Db 61 AGACCAAGGAGACAGTGTGTGCAAGAGACTGTGTGTGTACCAAGTGTGCAATTATGAAGAAAA 120

QY 124 GGAACAAATATGCCGATGCGCAAGGGGTGATGACATGATGATTACTGCAATGGC 177

Db 121 GGAACAGTATGCCGATAGCAAGGGGTGATGACATGATGATTACTGCAATGGC 174

RESULT 13
AAQ50390
ID AAQ50390 standard; cDNA to mRNA; 174 BP.

AC AAQ50390;

DT 24-OCT-2003 (revised)

DT 11-MAY-1994 (first entry)

DE Platelet aggregation inhibitory peptide.

KW Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF; ss.

OS Gloydius halys blomhoffi.

PN JP05255395-A.

PD 05-OCT-1993.

```

XX 03-OCT-1991; 91JP-00256234.
XX
XX 26-OCT-1990; 90JP-00287116.
XX
XX 20-FEB-1991; 91JP-00026328.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX WPI; 1993-348481/44.
XX
XX P-PSDB; AAR42863.
XX
XX Polypeptide of specified aminoacid sequence - used for inhibiting
XX platelet aggregation caused by e.g. collagen, thrombin, etc.
XX
XX Example; Page 30; 50pp; Japanese.
XX
XX The sequence is that encoding a polypeptide which inhibits platelet
XX aggregation caused by ADP, collagen, thrombin, arachidonic acid and PAF.
XX (Updated on 24-OCT-2003 to standardise OS field)
XX
XX Sequence 174 BP; 50 A; 32 C; 55 G; 37 T; 0 U; 0 Other;
XX
Query Match 71.2%; Score 151.6; DB 2; Length 174;
Best Local Similarity 92.0%; Pred. No. 1.5e-41;
Matches 160; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 4 GAAGATGTGACTGTGGCGCTCTCTGCAAAATCCGTGCTGCGATGCTGCAACCTGTAAACTG 63
DB 1 GAGGACTGCGACTGTGGCTCTCTCTGCAAAATCCGTGCTGTATGCTGCAACCTGTAAACTG 60
QY 64 AGACCAAGGCGCGCACTGTGCAAGAGACTGTGTGTGACCAAGTCAATTTATGAAGAA 123
DB 61 AGACCAAGAGCAAGCTGTGCAAGAGACTGTGTGTGACCAAGTCAATTTATGAAGAA 120
QY 124 GAACATATATGCGCGATGCGCAAGGGGTATGATGATGATTAATCTGCAATGCG 177
DB 121 GGAACAGTATGCCGATAGCAAGGGGTATGATGATGATTAATCTGCAATGCG 174

RESULT 14
AAQ50384
ID AAQ50384 standard; cDNA to mRNA; 174 BP.
XX
XX AAQ50384;
XX
XX 24-OCT-2003 (revised)
XX
XX 11-MAY-1994 (first entry)
XX
XX Platelet aggregation inhibitory peptide.
XX
XX Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF; ss.
XX
XX Gloydins hays blomhoffi.
XX
XX JP05255395-A.
XX
XX 05-OCT-1993.
XX
XX 03-OCT-1991; 91JP-00256234.
XX
XX 26-OCT-1990; 90JP-00287116.
XX
XX 20-FEB-1991; 91JP-00026328.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX WPI; 1993-348481/44.
XX
XX P-PSDB; AAR42857.
XX
XX Polypeptide of specified aminoacid sequence - used for inhibiting
XX platelet aggregation caused by e.g. collagen, thrombin, etc.
XX
XX Example; Page 27; 50pp; Japanese.

```

```

CC The sequence is that encoding a polypeptide which inhibits platelet
CC aggregation caused by ADP, collagen, thrombin, arachidonic acid and PAF.
CC (Updated on 24-OCT-2003 to standardise OS field)
XX
XX Sequence 174 BP; 50 A; 31 C; 54 G; 39 T; 0 U; 0 Other;
XX
Query Match 71.2%; Score 151.6; DB 2; Length 174;
Best Local Similarity 92.0%; Pred. No. 1.5e-41;
Matches 160; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 4 GAAGATGTGACTGTGGCGCTCTCTGCAAAATCCGTGCTGCGATGCTGCAACCTGTAAACTG 63
DB 1 GAGGACTGCGACTGTGGCTCTCTCTGCAAAATCCGTGCTGTATGCTGCAACCTGTAAACTG 60
QY 64 AGACCAAGGCGCGCACTGTGCAAGAGACTGTGTGTGACCAAGTCAATTTATGAAGAA 123
DB 61 AGACCAAGAGCAAGCTGTGCAAGAGACTGTGTGTGACCAAGTCAATTTATGAAGAA 120
QY 124 GAACATATATGCGCGATGCGCAAGGGGTATGATGATGATTAATCTGCAATGCG 177
DB 121 GGAACAGTATGCCGATAGCAAGGGGTATGATGATGATTAATCTGCAATGCG 174

RESULT 15
AAQ44934
ID AAQ44934 standard; cDNA; 174 BP.
XX
XX AAQ44934;
XX
XX 24-OCT-2003 (revised)
XX
XX 11-MAY-1994 (first entry)
XX
XX pAgalpa3-101 platelet aggregation inhibitory polypeptide.
XX
XX Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF; ss.
XX
XX Gloydins hays blomhoffi.
XX
XX JP05255395-A.
XX
XX 05-OCT-1993.
XX
XX 03-OCT-1991; 91JP-00256234.
XX
XX 26-OCT-1990; 90JP-00287116.
XX
XX 20-FEB-1991; 91JP-00026328.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX WPI; 1993-348481/44.
XX
XX P-PSDB; AAR46948.
XX
XX Polypeptide of specified aminoacid sequence - used for inhibiting
XX platelet aggregation caused by e.g. collagen, thrombin, etc.
XX
XX Example; Fig 14; 50pp; Japanese.
XX
XX The sequence is that of pAgalpa3-101 cDNA which comprises a polypeptide
XX isolated from Agkistrodon hays blomhoffi. It was used in the isolation
XX and prodn. of a polypeptide inhibiting platelet aggregation caused by
XX ADP, collagen, thrombin, arachidonic acid and PAF. (Updated on 24-OCT-
XX 2003 to standardise OS field)
XX
XX Sequence 174 BP; 49 A; 32 C; 54 G; 39 T; 0 U; 0 Other;
XX
Query Match 70.4%; Score 150; DB 2; Length 174;
Best Local Similarity 91.4%; Pred. No. 5.2e-41;
Matches 159; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 4 GAAGATGTGACTGTGGCGCTCTCTGCAAAATCCGTGCTGCGATGCTGCAACCTGTAAACTG 63
DB 1 GAGGACTGCGACTGTGGCTCTCTCTGCAAAATCCGTGCTGTATGCTGCAACCTGTAAACTG 60

```


QY 64 AGACCAAGGGGCGCACTGTGTGCAAGAGACTGTGTGTGACCACTGCAGATTTATGAAGAA 123
DB 61 AGACAAAGGAGCACAAGTGTGCAAGAGACTGTGTGTGACCACTGCAGATTTTAAAAAA 120
QY 124 GGAACATATGCGGATGCAAGGGGTGATGACATGGATGATTAAGCAATGGC 177
DB 121 GGAACATATGCGGATGCAAGGGGTGATGACATGGATGATTAAGCAATGGC 174

Search completed: December 3, 2004, 18:47:15
Job time : 409 secs

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Patent No. 6710030
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
TITLE OF INVENTION: CONTORESTININ (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
FILE REFERENCE: 1279-338C3/09801388
CURRENT APPLICATION NUMBER: US/09/460,295B
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/163,047
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent version 3.1
SEQ ID NO 1
LENGTH: 2029
TYPE: DNA
ORGANISM: Agkistrodon contortrix
US-09-460-295B-1

Query Match 89.5%; Score 190.6; DB 4; Length 2029;
Best Local Similarity 93.4%; Pred. No. 8.8e-56;
Matches 199; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GGAGAGATGATGCTGGCGCTCCGCAAAATCCGTCGCGATGCTGCAACCTGAAA 60
DB 1323 GGAGAGAAATGATGCTTGAAGCTCTCCCAATCCGTCGCGATGCTGCAACCTGAAA 1382
QY 6T CTGAGACCGAGGGCGCGACAGTGTGCAAGAGACTGTGTGTGACAGTCCAGATTATGAAA 120
DB 1383 CTGACACAGAGGTACAGAGTGTGACAGATGAGACTGTGTGTGACAGTCCAGATTATGAAA 1442
QY 121 GAAGAACATATGCGCGATGCGCAAGGGGTGATGACATGATGATGCTGCAATGGCATA 180
DB 1443 GAAGAACATATGCGCGATGCGCAAGGGGTGATGACATGATGATGCTGCAATGGCATA 1502
QY 181 TCTGCTGCTGCTCCGAGAAATCCCTTCATGCC 213
DB 1503 TCTGCTGCTGCTCCGAGAAATCCCTTCATGCC 1535

RESULT 3
US-08-745-603-1
Sequence 1, Application US/08745603
Patent No. 5814609

GENERAL INFORMATION:
APPLICANT: Francis S. Markland, Jr.
TITLE OF INVENTION: COMPOSITIONS CONTAINING A DISINTEGRIN AND METHODS FOR
TITLE OF INVENTION: ITS USE IN PREVENTING METASTASIS AND OTHER CONDITIONS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berlin & Carson
STREET: 201 No. 5814609th Figueroa Street, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: ASCII DOS/TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/745,603
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Robert Berlin
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 1920-338C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213/977-1001
TELEFAX: 213/977-1003
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 911 base pairs (111 amino acids)
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-745-603-1

Query Match 78.4%; Score 167; DB 1; Length 911;
Best Local Similarity 94.5%; Pred. No. 8.4e-48;
Matches 173; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 31 AATCCGTGCTGCGATGCTGCAACCTGTAACTGAGACCGAGGCGCACTGTGCAAGAGA 90
DB 235 AATCCGTGCTGCGATGCTGCAACCTGTAACTGAGACCGAGGCGCACTGTGCAAGAGA 294
QY 91 CTGTGTGACCATGAGATTATGAAAGAAAGAAATATGCGGATGCGCAAGGCT 150
DB 295 CTGTGTGACCATGAGATTATGAAAGAAAGAAATATGCGGATGCGCAAGGCT 354
QY 151 GATGACATGATGATTAATGCAATGCAATATCTGCTGCTGCTCCAGAAATCCCTTCAT 210
DB 355 GATGACATGATGATTAATGCAATGCAATATCTGCTGCTGCTCCAGAAATCCCTTCAT 414
QY 211 GCC 213
DB 415 GCC 417

RESULT 4
5182260-22

Patent No. 5182260
APPLICANT: MARAGANORE, JOHN M.; JAKUBOWSKI, JOSEPH A.
TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
THOSE INHIBITORS AND COMPOSITIONS USING THEM
NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,313
FILING DATE: 01-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 303,585
FILING DATE: 27-JAN-1989
APPLICATION NUMBER: 303,590
FILING DATE: 27-JAN-1989
SEQ ID NO: 22
LENGTH: 219
5182260-22

Query Match 59.1%; Score 125.8; DB 6; Length 219;
Best Local Similarity 75.1%; Pred. No. 7.1e-34;
Matches 157; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GGAGAGAAATGATGCTGCGCTCTGCAAAATCCGTCGCGATGCTGCAACCTGTAAA 60
DB 10 GGTGAAGAAATGATGCTGCGCATCCCGGAAAAACCGTGCTCGACGCGGCCACCTGCAAA 69
QY 61 CTGAGACCGAGGGCGCGACAGTGTGCAAGAGACTGTGTGTCACAGTGAGATTATGAAA 120
DB 70 CTGCTCGGAGTGCACAGTGTGCAAGAGCTGTGTCTCGACAGTGCAATTATGAAA 129
QY 121 GAAGAACATATGCGCGATGCGCAAGGGGTGATGATGATGATTAATGCAATGGCATA 180
DB 130 GAAGAACATATGCGCGATGCGCAAGGGGTGATGATGATGATTAATGCAATGGCATA 189
QY 181 TCTGCTGCTGCTCCGAGAAATCCCTTCGA 209
DB 190 TCTGCTGCTGCTCCGAGAAATCCCTTCGA 218

RESULT 5
5182260-1

Patent No. 5182260
APPLICANT: VARAGANORE, JOHN M.; JAKUBOWSKI, JOSEPH A.
TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
THOSE INHIBITORS AND COMPOSITIONS USING THEM
NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,313
FILING DATE: 01-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 303,585
FILING DATE: 27-JAN-1989
APPLICATION NUMBER: 303,590
FILING DATE: 27-JAN-1989
SEQ ID NO: 1:
LENGTH: 226
5182260-1

Query Match: 59.1%; Score 125.8; DB 6; Length 226;
Best Local Similarity 75.1%; Pred. No. 7.2e-34;
Matches 157; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GGAGAAAGATGTGACTGTGGGCTCTGCAAAATCCGTGCTGAGTGTGCAACCTGTAA 60
DB 11 GGTAAAGATGCGACTGCGATCCCGGAAAACCCGTGCTGCAAGCGGCGACCTGCA 70
QY 61 CTGAGACCAAGGCGCGAGTGTGCAAGAGACTGTGTTGTGACCACTGCAATTATGAA 120
DB 71 CTGTGTCGGGTGACAGTGTGCAAGAGTGTGCTGCGACACAGTCAATTATGAA 130
QY 121 GAAGAAACAATATGCGGATGCAAGGAGTGTGATGATGATGATGATGATGATGATGAT 180
DB 131 GAAGGTACCGTTTCCGTCGCTGCTGAGGTGACAGCTTAACGACTTCAACGGTATC 190
QY 181 TCTGCTGCTGTCCGAGAAATCCCTTCCA 209
DB 191 TCTGCAAGTTCGCCGCGTAACCCGTTCCA 219

RESULT 6
US-07-623-611-11
Sequence 11, Application US/07623611
Patent No. 5242810
GENERAL INFORMATION:
APPLICANT: Maraganore, John M.
APPLICANT: Chao, Betty H.
APPLICANT: Strauch, Kathryn L.
APPLICANT: Thompson, Jeffrey S.
TITLE OF INVENTION: BIFUNCTIONAL INHIBITORS OF THROMBIN AND
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue - 29th Floor
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/623,611
FILING DATE: 19901207
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 715-0600

TELEFAX: (212) 715-0674
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: N
ANTI-SENSE: N
US-07-623-611-11

Query Match: 56.3%; Score 120; DB 1; Length 288;
Best Local Similarity 72.5%; Pred. No. 8.1e-32;
Matches 153; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 GGAGAAAGATGTGACTGTGGGCTCTGCAAAATCCGTGCTGAGTGTGCAACCTGTAA 60
DB 7 GGTAAAGATGCGACTGCGATCCCGGAAAACCCGTGCTGCAAGCGGCGACCTGCA 66
QY 61 CTGAGACCAAGGCGCGAGTGTGCAAGAGACTGTGTTGTGACCACTGCAATTATGAA 120
DB 67 CTGCTCCGGGTGCTCAAGTGTGCAAGTGTGCTGCTGCAACAGTCAATTATGAA 126
QY 121 GAAGAAACAATATGCGGATGCAAGGAGTGTGATGATGATGATGATGATGATGATGAT 180
DB 127 GAAGGTACCGTTTCCGTCGCTGCTGAGGTGACAGCTTAACGACTTCAACGGTATC 186
QY 181 TCTGCTGCTGTCCGAGAAATCCCTTCCATG 211
DB 187 TCTGCAAGTTCGCCGCGTAACCCGTTCCAAG 217

RESULT 7
PCT-US91-09108-11
Sequence 11, Application PC/TUS9109108
GENERAL INFORMATION:
APPLICANT: Biogen, Inc.
TITLE OF INVENTION: *BIFUNCTIONAL INHIBITORS OF THROMBIN AND PLATELET ACTIVAT
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue - 29th Floor
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/09108
FILING DATE: 19911205
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 715-0600
TELEFAX: (212) 715-0674
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: N

ANTI-SENSE: N
PCT-US91-09108-11

Query Match 56.3%; Score 120; DB 5; Length 288;
Best Local Similarity 72.5%; Pred. No. 8.1e-32;
Matches 153; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 GGAGAAAGATGTGACTGTGGCGCTCCCTGCAAAATCCGTCGCGATGCTGCAACCTGTAAA 60
DB 7 GGAGAAAGATGTGACTGTGGCGATTCCTCGAAAAACCCGTGCGACGACCTGCTACTGCAAA 66
QY 61 CTGAGACCAAGGCGCGACGTGTGACAGAGACTGTGTGTGACCAAGTCAGATTATGAAA 120
DB 67 CTGCGTCCGGGTGCTCAAGTCGCGTGAAGTCTGTGTGCGACCAAGTCGAATTCNNAAA 126
QY 121 GAAGAACAAATATCCCGATGCGAAGGGGTATACATGATGATTTACTGCAATGCATA 180
DB 127 GAAGGTACCGTTTGGCGGTGCTGTGTGTGACGACGTAAAGCTACTGCAACGGTATC 186
QY 181 TCTGCTGGCTGTCCAGAAATCCCTTCATG 211
DB 187 TCTGAGGTTCCTCCGCGTAACCGCTTCCACG 217

RESULT 8
US-07-623-611-10
Sequence 10, Application US/07623611

Patent No. 5242810

GENERAL INFORMATION:

APPLICANT: Marganore, John M.

APPLICANT: Chao, Betty H.

APPLICANT: Strauch, Kathryn L.

APPLICANT: Thompson, Jeffrey S.

TITLE OF INVENTION: BIFUNCTIONAL INHIBITORS OF THROMBIN AND

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Neave

STREET: 875 Third Avenue - 29th Floor

CITY: New York

STATE: New York

COUNTRY: United States

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/623,611

FILING DATE: 19901207

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: B154

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 715-0600

TELEFAX: (212) 715-0674

TELEX: 14-8367

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 288 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: N

ANTI-SENSE: N

US-07-623-611-10

Query Match 56.2%; Score 119.6; DB 1; Length 288;
Best Local Similarity 72.7%; Pred. No. 1.1e-31;

Matches 152; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 1 GGAGAAAGATGTGACTGTGGCGCTTCCTGCAAAATCCGTCGCGATGCTGCAACCTGTAAA 60
DB 79 GGAGAAAGATGTGACTGTGGCGATTCCTCGAAAAACCCGTGCGACGACCTGCTACTGCAAA 138
QY 61 CTGAGACCAAGGCGCGACGTGTGACAGAGACTGTGTGTGACCAAGTCAGATTATGAAA 120
DB 139 CTGCGTCCGGGTGCTCAAGTCGCGTGAAGTCTGTGTGCGACCAAGTCGAATTCNNAAA 198
QY 121 GAAGAACAAATATCCCGATGCGAAGGGGTATACATGATGATTTACTGCAATGCATA 180
DB 199 GAAGGTACCGTTTGGCGGTGCTGTGTGTGACGACGTAAAGCTACTGCAACGGTATC 258
QY 181 TCTGCTGGCTGTCCAGAAATCCCTTCGA 209
DB 259 TCTGAGGTTCCTCCGCGTAACCGCTTCCCA 287

RESULT 9
PCT-US91-09108-10
Sequence 10, Application PC/TUS9109108

GENERAL INFORMATION:

APPLICANT: Biogen, Inc.

TITLE OF INVENTION: * , BIFUNCTIONAL INHIBITORS OF THROMBIN AND PLATELET ACTIVAT

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Neave

STREET: 875 Third Avenue - 29th Floor

CITY: New York

STATE: New York

COUNTRY: United States

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/09108

FILING DATE: 19911205

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: B154

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 715-0600

TELEFAX: (212) 715-0674

TELEX: 14-8367

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 288 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: N

ANTI-SENSE: N

PCT-US91-09108-10

Query Match 56.2%; Score 119.6; DB 5; Length 288;
Best Local Similarity 72.7%; Pred. No. 1.1e-31;
Matches 152; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 1 GGAGAAAGATGTGACTGTGGCGCTTCCTGCAAAATCCGTCGCGATGCTGCAACCTGTAAA 60
DB 79 GGAGAAAGATGTGACTGTGGCGATTCCTCGAAAAACCCGTGCGACGACCTGCTACTGCAAA 138
QY 61 CTGAGACCAAGGCGCGACGTGTGACAGAGACTGTGTGTGACCAAGTCAGATTATGAAA 120
DB 139 CTGCGTCCGGGTGCTCAAGTCGCGTGAAGTCTGTGTGCGACCAAGTCGAATTCNNAAA 198

NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,001A
FILING DATE: 18-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15293B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2050 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 78..1940
US-09-026-001A-5

Query Match 41.8%; Score 89; DB 4; Length 2050;
Best Local Similarity 69.7%; Pred. No. 9.9e-21;
Matches 154; Conservative 0; Mismatches 55; Indels 12; Gaps 2;

QY 1 GGAGGAAGATGTCAGTGGCGCTCTG-----CAATCGTGCTGGATGTCGA 51
DB 1332 GGAGGAAGATGTCAGTGGCGCTCTCTGAGATTGTCAAAATACCTGCTGATGCTGCA 1391
QY 52 ACCGTAACTGAGACCAAGGGCGGAGTGCAGAGGACTGTGTGACCACTGAGA 111
DB 1392 ACTGTAACTGAGACATGAGGCGACAGTGTACTGTGAGAGTGTGTGAGAAATGCAAA 1451
QY 112 TTATGAAGAAGAACATATGCCGATGCGCAAGGGGTGA---TGAATGATGATTAC 168
DB 1452 TTATGAAGAGGAGGAGGAGATGCCGGGCGACAAAGATGATGCTGACTTCTGAACTC 1511
QY 169 TGCATGGCATATCTGCTGGCTGCTGCCCAAGAAATCCCTTCCA 209
DB 1512 TGCATGGCGCATCTGCTGTAAGTGTCCCAAGACAGCTTCCA 1552

RESULT 14
US-09-026-001A-9
Sequence 9, Application US/09026001A
Patent No. 6413760
GENERAL INFORMATION:
APPLICANT: Boonhoo, Amechand
APPLICANT: Seehra, Jasbir
APPLICANT: Shaw, Gray
APPLICANT: Sako, Dianne
TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge

STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,001A
FILING DATE: 18-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15293B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2335 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-026-001A-9

Query Match 41.8%; Score 89; DB 4; Length 2335;
Best Local Similarity 69.7%; Pred. No. 1.1e-20;
Matches 154; Conservative 0; Mismatches 55; Indels 12; Gaps 2;

QY 1 GGAGGAAGATGTCAGTGGCGCTCTG-----AAATCGTGCTGGAGTGTGCA 51
DB 1321 GGAGGAAGATGTCAGTGGCGCTCTCTGCGATTGTCAAAGGCTGTGGAACCTTCA 1380
QY 52 ACCGTAACTGAGACCAAGGGCGGAGTGCAGAGGACTGTGTGACCACTGAGA 111
DB 1381 ACTGTAACTGAGACCACTGATGACAGTGTACTCCGAAGGCTGTGTGAGAAATGCAAA 1440
QY 112 TTATGAAGAAGAACATATGCCGATGCGCAAGGGGTGA---TGAATGATGATTAC 168
DB 1441 TTATGAAGGAGGAGGAGGAGAAATGCCGGGCGACAAAGATGATGCTGACTTCTGAACTC 1500
QY 169 TGCATGGCATATCTGCTGGCTGCTGCCCAAGAAATCCCTTCCA 209
DB 1501 TGCATGGCGCATCTGCTGTAAGTGTCCCAAGACAGCTTCCA 1541

RESULT 15
US-09-026-001A-17
Sequence 17, Application US/09026001A
Patent No. 6413760
GENERAL INFORMATION:
APPLICANT: Boonhoo, Amechand
APPLICANT: Seehra, Jasbir
APPLICANT: Shaw, Gray
APPLICANT: Sako, Dianne
TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25


```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,001A
FILING DATE: 18-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15293B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2359 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-026-001A-17

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Query Match 41.8%; Score 89; DB 4; Length 2359;
Best Local Similarity 69.7%; Pred. No. 1,1e-20;
Matches 154; Conservative 0; Mismatches 55; Indels 12; Gaps 2;

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QY 1 GGAGAGAGATGTGACTGTGGGCTTCCTGC-----AAATCGGTGCTGGATGCTGCA 51
    |||
DB 1345 GGAGAGAGATGTGACTGTGGGCTTCCTGCAGATTGTCAAGTGCCTGCTCGAGCTPACA 1404
    |||
QY 52 ACCTGTAACCTGAGACCGAGGCGCAGTGTGCAGAGAGACTGTGTGTGACCAAGTGCAGA 111
    |||
DB 1405 ACTGTAACTACACACCTCATGCACAGTGTGACTCCGAGAGGTGTGTGAGAAATGCA 1464
    |||
QY 112 TTTATGAAAGAGAGACATATGCCGATGCGCAAGGCTGA---TGACATGATGATTAC 168
    |||
DB 1465 TTTAAGGAGAGAGAGAGATGCGGCGCAGCAAGAGATGATGTGACTTGCTGAACTC 1524
    |||
QY 169 TGCATGCGCATATCTGCTGGCTGTCCCAAGAAATCCCTTCCA 209
    |||
DB 1525 TGCACTGGCCCAATCTGCTGAGTGTCCCAAGACATCTTCCA 1565
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Search completed: December 3, 2004, 20:10:12
 Job time : 90 secs

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GenCore version 5.1.6
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OK nucleic - nucleic search, using sw model

Run on: December 3, 2004, 18:11:26 ; Search time 2974 Seconds

(without alignments)
2609,840 Million cell updates/sec

Title: US-10-089-473A-2

Perfect score: 1 ggagaagaatgcactgctg.....ccagaatccctccatgc 213

Sequence: 1 ggagaagaatgcactgctg.....ccagaatccctccatgc 213

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3282875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	182.6	85.7	409	4	EM401624 JLD07F S
2	180.6	84.8	399	4	EM401419 GH063F S
3	101.2	47.5	476	4	EM401547 JH012F S
4	100.4	47.1	444	4	EM401444 JH1A0F S
5	100.2	47.0	357	4	EM401492 JH2B0F S
6	100.2	47.0	432	4	EM401556 JH3F0F S
7	98.2	46.1	377	4	EM401456 JH1C0F S
8	74.6	35.0	420	4	EM401655 JLD03F S
9	68.2	32.0	411	4	EM401433 GH089F S
10	68.2	32.0	474	4	EM401391 GH010F S
11	68.2	32.0	527	4	EM401397 GH020F S
12	68.2	32.0	542	4	EM401405 GH029F S
13	68.2	32.0	565	4	EM401393 GH016F S
14	60.6	28.5	845	7	CF377167 AGENCOURT
15	60.6	28.5	863	7	A1525705 PT1.3_04
16	58.4	27.4	519	1	AL783368 AL783368
17	55.6	26.1	384	4	EM401619 JLD10F S
18	54.8	25.7	846	7	CK596457 AGENCOURT
19	54	25.4	396	1	A2280392 Zr04b0.4
20	54	25.4	593	6	CD535662 Leukons.7
21	52.4	24.6	549	2	BE389727 601281979
22	52.4	24.6	603	2	BE389822 601282620
23	52.4	24.6	635	2	BE388453 601285592
24	52.4	24.6	706	2	BE389752 601282919

25	52.4	24.6	968	2	BE410120 601302417
26	52.4	24.6	3108	3	AF326918 Homo sapi
27	51.2	24.0	572	2	BE390985 601283174
28	50.4	23.7	620	5	BX670023 BX670023
29	50.4	23.7	690	5	BX670024 BX670024
30	50.4	23.7	852	6	CD361846 AGENCOURT
31	48.8	22.9	366	4	BG000250 MR3-GN022
32	48.8	22.9	643	4	BM538117 hsa9011.9
33	48.4	22.7	955	5	BX336226 BX336226
34	47.8	22.4	707	1	AU136809 AU136809
35	47.6	22.3	450	2	AM605922 RCI-HT025
36	47.4	22.3	727	1	AU127125 AU127125
37	47.2	22.2	335	2	BF771395 IL5-IT002
38	47.2	22.2	340	1	AA368597 EST60160
39	47.2	22.2	362	5	BQ368056 QV0-GN014
40	47.2	22.2	375	1	AA368827 EST80139
41	47.2	22.2	383	4	BF987229 QV0-GN014
42	47.2	22.2	388	6	CI8735 CI8735 Huma
43	47.2	22.2	401	5	BQ367967 PM4-GN051
44	47.2	22.2	404	4	BG012562 IL5-GN023
45	47.2	22.2	411	7	T34209 ya30c07.12

ALIGNMENTS

RESULT 1
EM401624 409 bp mRNA linear EST 01-MAY-2002
LOCUS JLD07F Snake Bothrops insularis library IL3 Bothrops insularis
DEFINITION CDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.
ACCESSION EM401624
VERSION EM401624.1 GI:20376252
KEYWORDS EST.
SOURCE Bothrops insularis (Island Jararaca)
ORGANISM Bothrops insularis
Bukaryoceta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
REFERENCE 1 (bases 1 to 409)
Tunqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of
the pitviper snake Bothrops insularis through the generation of
expressed sequence tags (ESTs)
JOURNAL Gene 299 (1-2), 279-291 (2002)
MEDLINE 22347338
PubMed 12459276
COMMENT Contact: Paulo Lee HO
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brasil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BTM08A (see Reference)
Seq primer: M13F.
Location/Qualifiers
1..409
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/feature_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL3"
/note="Organ: Venom glands; Vector: pGEM11zf+; Site 1: Eco
RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (Life Technologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11zf+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or

ORIGIN cluster was obtained through Blast searches (e-value < e-05)."

Query Match 85.7%; Score 182.6; DB 4; Length 409;
Best Local Similarity 91.1%; Pred. No. 1.2e-45;
Matches 194; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 GGAGAAAGATGTGATGTGGCGCTCTCTCAATCCGTCGCTGCACTGTAA 60
DB 85 GGAGAAAGATGTGATGTGGCGCTCTCTCAATCCGTCGCTGCACTGTAA 144
QY 61 CTGAGACCAAGGCGCAGTGTGACAGAGACTGTGTGTGACAGTGTGATA 120
DB 145 CTGAGACCAAGGCGCAGTGTGACAGAGACTGTGTGTGACAGTGTGATA 204
QY 121 GAAGAACAAATATGCGCGAGTGGCAAGGGGTATGACATGATGATTA 180
DB 205 GGAGAAAGATGTGATGTGGCGCTCTCTCAATCCGTCGCTGCACTGTAA 264
QY 181 TCTGCTGCTGCTCCAGAAATCCCTTCATGCC 213
DB 265 TCTGCTGCTGCTCCAGAAATCCCTTCATGCC 297

RESULT 2 399 bp mRNA linear EST 01-MAY-2002
LOCUS BM401419
DEFINITION GH063F Snake Bothrops insularis library I12 Bothrops insularis cDNA
5' similar to Snake venom metalloproteinase, mRNA sequence.
ACCESSION BM401419 GI:20376047
VERSION BM401419.1
KEYWORDS EST.
SOURCE Bothrops insularis (Island Jararaca)
ORGANISM Bothrops insularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.

REFERENCE 1 (bases 1 to 399)
Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of
the pitviper snake Bothrops insularis through the generation of
expressed sequence tags (ESTs)

JOURNAL Gene 289 (1-2), 279-291 (2002)

MEDLINE 22347338

PUBMED 12459276

COMMENT

Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITW08A (see Reference)
Seq primer: M13F.

FEATURES
source location/Qualifiers

1..399
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library I12"
/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (Life Technologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11zf+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <

ORIGIN e-05)."

Query Match 84.8%; Score 180.6; DB 4; Length 399;
Best Local Similarity 90.1%; Pred. No. 5e-45;
Matches 192; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 GGAGAAAGATGTGATGTGGCGCTCTCTCAATCCGTCGCTGCACTGTAA 60
DB 108 GGAGAAAGATGTGATGTGGCGCTCTCTCAATCCGTCGCTGCACTGTAA 167
QY 61 CTGAGACCAAGGCGCAGTGTGACAGAGACTGTGTGTGACAGTGTGATA 120
DB 168 CTGAGACCAAGGCGCAGTGTGACAGAGACTGTGTGTGACAGTGTGATA 227
QY 121 GAAGAACAAATATGCGCGAGTGGCAAGGGGTATGACATGATGATTA 180
DB 228 GGAGAAAGATGTGATGTGGCGCTCTCTCAATCCGTCGCTGCACTGTAA 287
QY 181 TCTGCTGCTGCTCCAGAAATCCCTTCATGCC 213
DB 288 TCTGCTGCTGCTCCAGAAATCCCTTCATGCC 320

RESULT 3 476 bp mRNA linear EST 01-MAY-2002
LOCUS BM401547
DEFINITION JH3D12F Snake Bothrops insularis library I13 Bothrops insularis
cDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.
ACCESSION BM401547 GI:20376175
VERSION BM401547.1
KEYWORDS EST.
SOURCE Bothrops insularis (Island Jararaca)
ORGANISM Bothrops insularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.

REFERENCE 1 (bases 1 to 476)
Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of
the pitviper snake Bothrops insularis through the generation of
expressed sequence tags (ESTs)

JOURNAL Gene 289 (1-2), 279-291 (2002)

MEDLINE 22347338

PUBMED 12459276

COMMENT

Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITW06A (see Reference)
Seq primer: M13F.

FEATURES
source location/Qualifiers

1..476
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library I13"
/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (Life Technologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11zf+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <

ORIGIN

Query Match 47.5%; Score 101.2; DB 4; Length 476;
Best Local Similarity 73.0%; Pred. No. 2,4e-20;
Matches 162; Conservative 0; Mismatches 48; Indels 12; Gaps 2;

QY 1 GGAGAAATGCTACTGTGGGCTCCCTG-----CAATCCGGTCCGATGTGGA 51
DB 208 GGAGAAATGCTACTGTGGGCTCCCTG-----CAATCCGGTCCGATGTGGA 267
QY 52 ACCTGTAATGAGACCGAGGCGCAGTGTGAGAAAGACTGTGTGTGACAGTCAGA 111
DB 268 ACGTGTAACTGAAATCAGGGTCAAGTGTGACATGAGACTGTGTGTGAGCAATGCAAA 327
QY 112 TTTATGAAAGAGAAATATGCGCGATGCGCAAGGGTGA---TGACATGATGATTAC 168
DB 328 TTTAGCAATCAGAAAGAAATGCGCGCATGATGATGATGATGACCCGCTGAACAC 387
QY 169 TGCATGCGATATCTGCTGCTGCTGCCAGAAATCCCTTCAT 210
DB 388 TGACATGCGCATCTCTGAGTGTCTGCGAGATGCTTCAT 429

RESULT 4 444 bp mRNA linear EST 01-MAY-2002
BM401444
LOCUS JH2B04F Snake Bothrops insularis library IJ3 Bothrops insularis
DEFINITION cDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.

ACCESSION BM401444.1 GI:20376072
VERSION BM401444
KEYWORDS EST.
SOURCE Bothrops insularis (Island Jararaca)
ORGANISM Bothrops insularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.

REFERENCE 1 (bases 1 to 444)
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

JOURNAL Gene 299 (1-2), 279-291 (2002)
MEDLINE 22347338
PubMed 12459276

COMMENT

Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br

This EST corresponds to cluster BTM30A (see Reference)
Seq primer: M13F.

FEATURES

source
1..444
Location/Qualifiers
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IJ3"
/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; 5'ug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."

Query Match 47.1%; Score 100.4; DB 4; Length 444;
Best Local Similarity 75.8%; Pred. No. 4.2e-20;
Matches 138; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

QY 31 AATCGTCTCGATGATGCTGCAACCTGTAATGAGACCGAGGCGCAGTGTGAGAAAGA 90
DB 30 AATCGTCTCGATGATGCTGCAACCTGTAATGAGACCGAGTGTGAAATCTGA 89
QY 91 CTGTGTGTGACCACTGCAATTTATGAAAGAGAAATATCCCGATGCGCAAGGGGT 150
DB 90 GAGTGTGTGACCACTGCAATTTAAGGACAGAGATCAGAAATCCGCTGCAAGAGAT 149
QY 151 GA---TGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 207
DB 150 GAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 209
QY 208 CA 209
DB 210 CA 211

RESULT 5 357 bp mRNA linear EST 01-MAY-2002
BM401492
LOCUS JH2B04F Snake Bothrops insularis library IJ3 Bothrops insularis
DEFINITION cDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.

ACCESSION BM401492
VERSION BM401492.1 GI:20376120
KEYWORDS EST.
SOURCE Bothrops insularis (Island Jararaca)
ORGANISM Bothrops insularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.

REFERENCE 1 (bases 1 to 357)
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

JOURNAL Gene 299 (1-2), 279-291 (2002)
MEDLINE 22347338
PubMed 12459276

COMMENT

Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BTM11A (see Reference)
Seq primer: M13F.

FEATURES

source
1..357
Location/Qualifiers
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IJ3"
/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; 5'ug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."

Query Match 47.0%; Score 100.2; DB 4; Length 357;
 Best Local Similarity 72.9%; Pred. No. 4.6e-20;
 Matches 161; Conservative 0; Mismatches 48; Indels 12; Gaps 2;

1 GGAGAGAAATGATGACTGTGGCGCTCTGCA-----ATCGTGTGGATGCTCA 51
 |||||
 56 GGAGAGAAATGATGACTGTGGCGCTCTGCA-----ATCGTGTGGATGCTCA 115
 |||||
 52 ACTGTAACTGAGACCGAGGCGCGAGTGTGCAGAGACTGTGTGACCACTGAGA 111
 |||||
 116 ACCTGTAACTGAGACCGAGGCGCGAGTGTGCAGAGACTGTGTGACCACTGAGA 175
 |||||
 112 TTTATGAAGAAGAGACCATATGCGGATGGCAGAGGCTGA---TGACATGATGATTAC 168
 |||||
 176 TTTAAAGACCGACATCGAATGCGGCGACAGAGAGTGTGACATGTGTGAAGC 235
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 169 TGCATGGCAATCTGCTGTGCTCCAGAAATCCCTTCCA 209
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 236 TGCATGGCAATCTGCTGTGCTCCAGAAATCCCTTCCA 276
 |||||

RESULT 6
 BM401556 432 bp mRNA linear EST 01-MAY-2002
 LOCUS JH3F08F Snake Bothrops insularis library IL3 Bothrops insularis
 DEFINITION CDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.
 ACCESSION BM401556
 VERSION BM401556.1 GI:20376184
 KEYWORDS EST.
 SOURCE Bothrops insularis (Island Jararaca)
 ORGANISM Bothrops insularis
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
 Viperidae; Crotalinae; Bothrops.
 1 (bases 1 to 432)
 JUNGUEIRA-DE-AZEVEDO, I.L.M. and HO, P.L.
 A survey of gene expression and diversity in the venom glands of
 the pitviper snake Bothrops insularis through the generation of
 expressed sequence tags (ESTs)
 JOURNAL Gene 299 (1-2), 279-291 (2002)
 MEDLINE 22347338
 PUBMED 12459276
 COMMENT Contact: Paulo Lee Ho
 Centro de Biotecnologia
 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BTM11A (see Reference)
 Seq primer: M13F.
 Location/Qualifiers
 source 1..432
 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /tissue_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL3"
 /note="Organ: venom glands; Vector: pGEM11zf+; Site: 1: Eco
 RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
 venom glands were primed with oligo-(dT) and reverse
 transcribed to cDNA using Superscript Plasmid System for
 cDNA Synthesis and Cloning (Life Technologies). The cDNAs
 were selected by size (350-600 pb and up 600 pb) in
 agarose gel electrophoresis, linked to Eco RI adapters and
 directionally cloned in pGEM11zf+ vector (Promega). ESTs
 were generated from random clones and grouped in unique
 sequences. The putative identification of each EST or
 cluster was obtained through Blast searches (e-value <
 e-05)."

ORIGIN

Query Match

47.0%; Score 100.2; DB 4; Length 432;

Best Local Similarity 72.9%; Pred. No. 4.8e-20;
 Matches 161; Conservative 0; Mismatches 48; Indels 12; Gaps 2;

1 GGAGAGAAATGATGACTGTGGCGCTCTGCA-----ATCGTGTGGATGCTCA 51
 |||||
 162 GGAGAGAAATGATGACTGTGGCGCTCTGCA-----ATCGTGTGGATGCTCA 241
 |||||
 52 ACTGTAACTGAGACCGAGGCGCGAGTGTGCAGAGACTGTGTGACCACTGAGA 111
 |||||
 242 ACCTGTAACTGAGACCGAGGCGCGAGTGTGCAGAGACTGTGTGACCACTGAGA 301
 |||||
 112 TTTATGAAGAAGAGACCATATGCGGATGGCAGAGGCTGA---TGACATGATGATTAC 168
 |||||
 302 TTTAAAGACCGACATCGAATGCGGCGACAGAGAGTGTGACATGTGTGAAGC 361
 |||||
 169 TGCATGGCAATCTGCTGTGCTCCAGAAATCCCTTCCA 209
 |||||
 362 TGCATGGCAATCTGCTGTGCTCCAGAAATCCCTTCCA 402
 |||||

RESULT 7
 BM401456 377 bp mRNA linear EST 01-MAY-2002
 LOCUS JH1C08F Snake Bothrops insularis library IL3 Bothrops insularis
 DEFINITION CDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.
 ACCESSION BM401456
 VERSION BM401456.1 GI:20376084
 KEYWORDS EST.
 SOURCE Bothrops insularis (Island Jararaca)
 ORGANISM Bothrops insularis
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
 Viperidae; Crotalinae; Bothrops.
 1 (bases 1 to 377)
 JUNGUEIRA-DE-AZEVEDO, I.L.M. and HO, P.L.
 A survey of gene expression and diversity in the venom glands of
 the pitviper snake Bothrops insularis through the generation of
 expressed sequence tags (ESTs)
 JOURNAL Gene 299 (1-2), 279-291 (2002)
 MEDLINE 22347338
 PUBMED 12459276
 COMMENT Contact: Paulo Lee Ho
 Centro de Biotecnologia
 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BTM06A (see Reference)
 Seq primer: M13F.
 Location/Qualifiers
 source 1..377
 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /tissue_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL3"
 /note="Organ: venom glands; Vector: pGEM11zf+; Site: 1: Eco
 RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
 venom glands were primed with oligo-(dT) and reverse
 transcribed to cDNA using Superscript Plasmid System for
 cDNA Synthesis and Cloning (Life Technologies). The cDNAs
 were selected by size (350-600 pb and up 600 pb) in
 agarose gel electrophoresis, linked to Eco RI adapters and
 directionally cloned in pGEM11zf+ vector (Promega). ESTs
 were generated from random clones and grouped in unique
 sequences. The putative identification of each EST or
 cluster was obtained through Blast searches (e-value <
 e-05)."

ORIGIN

Query Match

46.1%; Score 98.2; DB 4; Length 377;

Best Local Similarity 72.6%; Pred. No. 2e-19;

Matches 159; Conservative 0; Mismatches 48; Indels 12; Gaps 2;

QY 4 GAAGAATGTGACTGTGGGGCTCTCTG-----CAATCCGTCGTCGATGTGCAC 54
 Db 1 GAAGAATGTGACTGTGGGGCTCTCTGAAATTTGTCAAAATGATGCTGCGATGCTGCACG 60
 QY 55 TGTAACTGAGACCAAGGGGCGGAGTGTGCAGAAAGACTGTGTTGTGAACCAATGCAATTT 114
 Db 61 TGTAACTGAGAAATCAGGGTCACTGTGACATGAAAGACTGTGTTGTGAGCAATGCAATTT 120
 QY 115 ATGAAGAAGAACAAATATGCGGAGATGCAAGGGGGTGA---TGACATGATGATTTCTGC 171
 Db 121 AGCAAAATCAGGACGAATGCGGGCATCAATGATGATGATGACCCGGCTGAACACTGC 180
 QY 172 AATGCATATCTGCTGTGGCTGTCCAGAAATCCCTTCAT 210
 Db 181 ACTGGCCATCTCTGTGAGTGTCTGTCGAGATGTCTTCAT 219

RESULT 8 420 bp mRNA linear EST 01-MAY-2002
 LOCUS BM401655
 DEFINITION J12E03F Snake Bothrops insularis library IL3 Bothrops insularis
 CDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.

ACCESSION BM401655
 VERSION BM401655.1 GI:20376283
 KEYWORDS EST.
 SOURCE Bothrops insularis (Island Jararaca)
 ORGANISM Bothrops insularis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Bothrops.

REFERENCE 1 (bases 1 to 420)
 A survey of gene expression and diversity in the venom glands of
 the pitviper snake Bothrops insularis through the generation of
 expressed sequence tags (ESTs)

JOURNAL 22347338
 MEDLINE Gene 299 (1-2), 279-291 (2002)
 PUBMED
 COMMENT Contact: Paulo Lee Ho
 Centro de Biotecnologia
 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BTM16A (see Reference)
 Seq primer: M13F.

FEATURES
 source 1..420
 Location/Qualifiers
 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /tissue_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL3"
 /note="Organ: Venom glands; Vector: pGEM11zf+; Site 1: Eco
 RI; Site 2: Not I; 5'ug of mRNA from Bothrops insularis
 venom glands were primed with oligo-(dT) and reverse
 transcribed to cDNA using Superscript Plasmid System for
 cDNA Synthesis and Cloning (Life Technologies). The cDNAs
 were selected by size (350-600 pb and up 600 pb) in
 agarose gel electrophoresis, linked to Eco RI adaptors and
 directionally cloned in pGEM11zf+ vector (Promega). ESTs
 were generated from random clones and grouped in unique
 sequences. The putative identification of each EST or
 cluster was obtained through Blast searches (e-value <
 e-05)."

ORIGIN

Query Match 35.0%; Score 74.6; DB 4; Length 420;
 Best Local Similarity 74.5%; Pred.No. 4.3e-12;
 Matches 108; Conservative 0; Mismatches 34; Indels 3; Gaps 1;

QY 68 CAGGGCGCAGTGTGCAGAGACTGTGTGTGACCAATGACATTTATGAAGAAGAA 127
 Db 5 CATGGGTAGAGTGAATCTGGAGAGTGTGTGACCAATGACATTTAAGGAGCAGAA 64
 QY 128 CAATATGCCCGATGCGCAAGGGGTGA---TGACATGATGATTACTGCAATATCTG 184
 Db 65 CAGATGCCCGGCGACCAAGAGTGTGTGACATTTGAAAGCTGACGCGCAATCTG 124
 QY 185 CTGGCTGTCCAGAAATCCCTTCCA 209
 Db 125 CTGACTGTCTCCACATGACTTCAA 149

RESULT 9 411 bp mRNA linear EST 01-MAY-2002
 LOCUS BM401433
 DEFINITION GH089F Snake Bothrops insularis library IL2 Bothrops insularis CDNA
 5' similar to Snake venom metalloproteinase, mRNA sequence.
 ACCESSION BM401433
 VERSION BM401433.1 GI:20376061
 KEYWORDS EST.
 SOURCE Bothrops insularis (Island Jararaca)
 ORGANISM Bothrops insularis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Bothrops.

REFERENCE 1 (bases 1 to 411)
 A survey of gene expression and diversity in the venom glands of
 the pitviper snake Bothrops insularis through the generation of
 expressed sequence tags (ESTs)

JOURNAL 22347338
 MEDLINE Gene 299 (1-2), 279-291 (2002)
 PUBMED
 COMMENT Contact: Paulo Lee Ho
 Centro de Biotecnologia
 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BTM06A (see Reference)
 Seq primer: M13F.

FEATURES
 source 1..411
 Location/Qualifiers
 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /tissue_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL2"
 /note="Organ: Venom glands; Vector: pGEM11zf+; Site 1: Eco
 RI; Site 2: Not I; 5'ug of mRNA from Bothrops insularis
 venom glands were primed with oligo-(dT) and reverse
 transcribed to cDNA using Superscript Plasmid System for
 cDNA Synthesis and Cloning (Life Technologies). The cDNAs
 were selected by size (350-600 pb and up 600 pb) in
 agarose gel electrophoresis, linked to Eco RI adaptors and
 directionally cloned in pGEM11zf+ vector (Promega). ESTs
 were generated from random clones and grouped in unique
 sequences. The putative identification of each EST or
 cluster was obtained through Blast searches (e-value <
 e-05)."

ORIGIN

Query Match 32.0%; Score 68.2; DB 4; Length 411;
 Best Local Similarity 69.9%; Pred.No. 4.2e-10;
 Matches 107; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

QY 61 CTGAGACCAAGGGCGCAGTGTGCAGAGACTGTGTGTGACCAATGACATTTATGAAA 120
 Db 1 CTGAATTCAGGGGTCAAGTGTGAGACATGAGACTGTGTGAGCAATGCAATTTGCAAA 60

Qy	Db	RESULT 10
Qy	121	GAAGAAACAATATGCCGATGCGAAGGGGTGA---TGCATGATGATGATTACTGCAATGAC 177
Db	61	TCAGGAACAGATGCCGGGACATCAATGATGATGTGACCCGGCTGAACACTGCACTGC 120
Qy	178	ATATCTGCTGCTGTGCCAAGAATCCCTTCAT 210
Db	121	CAATCCTGTGAGTGTGCTGACAGATGTCTTCAT 153
LOCUS		BM401391 474 bp linear EST 01-MAY-2002
DEFINITION		GH010F Snake Bothrops insularis library IL2 Bothrops insularis cDNA
ACCESSION		5' similar to Snake venom metalloproteinase, mRNA sequence.
VERSION		BM401391
KEYWORDS		BM401391.1 GI:20376019
SOURCE		EST.
ORGANISM		Bothrops insularis (island jararaca)
		Bothrops insularis
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
		Viperidae; Crotalinae; Bothrops.
REFERENCE		1 (bases 1 to 474)
AUTHORS		Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
TITLE		A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)
JOURNAL		Gene 299 (1-2), 279-291 (2002)
MEDLINE		22347338
PUBMED		12459226
COMMENT		Contact: Paulo Lee Ho Centro de Biotecnologia Instituto Butantan Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900 Tel: 55 11 37 26 7222 ext. 2003 Fax: 55 11 37 26 1505 Email: hoplees@usp.br This EST corresponds to cluster BTM06A (see Reference) Seq primer: M13F.
FEATURES		Location/Qualifiers
source		1..474
		/organism="Bothrops insularis"
		/mol_type="mRNA"
		/db_xref="taxon:8723"
		/tissue_type="venom glands"
		/clone_lib="Snake Bothrops insularis library IL2"
		/note="Organ: venom glands; Vector: pGEM11zf+; Site: 1; Eco RI; Site 2: Not I; 5ug of mRNA from Bothrops insularis venom glands were primed with oligo-(dG) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."
ORIGIN		
		32.0%; Score 68.2; DB 4; Length 474;
		Best Local Similarity 69.9%; Pred. No. 4.3e-10;
		Matches 107; Conservative 0; Mismatches 43; Indels 3; Gaps 1;
Qy	61	CTGAGACAGGGGGCGCACTGTGCAGAAAGACTGTGTTGTGACCGTGCAGATTTATGAA 120
Db	1	CTGAATACAGGCTACACAGTGTGACATGAGACACTGTGTGTGACATGCAAATTTAGCAA 60
Qy	121	GAAGAAACAATATGCCGATGCGAAGGGGTGA---TGCATGATGATGATTACTGCAATGAC 177
Db	61	TCAGGAACAGATGCCGGGACATCAATGATGATGTGACCCGGCTGAACACTGCACTGC 120
Qy	178	ATATCTGCTGCTGTGCCAAGAATCCCTTCAT 210
Db	121	CAATCCTGTGAGTGTGCTGACAGATGTCTTCAT 153

Db

|-----||---|
121 CAATCTGTAGTGTCTCGACGATGTTTCAT 153

RESULT 11

BMA01397
LOCUS
DEFINITION GH020F Snake Bothrops insularis library IL2 Bothrops insularis cDNA sequence.

ACCSSION BMA01397
VERSION BMA01397.1 GI:20376025
KEYWORDS EST.
SOURCE Bothrops insularis (Island Jarakaca)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidodontaia; Squamata; Scleroglossa; Serpentes; Colubroidae;
Viperidae; Crotalinae; Bothers.

REFERENCE Junqueira-de-Azevedo, I.L.N., and Ho, P.J.
AUTHORS A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

TITLE Gene 299 (1-2), 279-281 (2002)

JOURNAL MEDLINE 22347338
PUBMED 12459276

COMMENT Contact: Paulo Lee Ho
Centro de Biocologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel.: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITW06A (see Reference)
Seq primer: M13f.

FEATURES

SOURCE Location/Qualifiers

1..527

/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref=taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL2"
/note=Torgans: venom glands; Vector: pGENM1zf+; Site_1: Eco RI, Site_2: Not I; Site_3: SacI from Bothrops insularis venom glands were primed with oligo-(d)T and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adaptors and directionally cloned in pCMVizf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."'

ORIGIN

Query Match 32.0%; Score 68.2; DB 4; Length 527;

Best Local Similarity 69.9%; Pred.No. 4.5e-10;

Matches 107; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Db 1 CTGAACAAGGGGCAGTGTCAGAAGCATGCTGTGTGTAACCAATATTATGAA 120
61 CTGAGACAGGGGCCAGTGTCAGAAGCATGCTGTGTGTAACCAATATTATGAA 120
Dg 1 CTGAACAAGGGGCAGTGTCAGAAGCATGACTGTGTGTAACCAATATTATGAAA 60
Cy 121 GAAGAACATATATCCCGCAGTAGCCAAGGCGTGA--TGACATGATGATTTACTGCAATGGC 177
Dg 61 TCAGAAAAAGAAAGTCCCAGGATCATATAGGAATGTACCCGGCTGAACACTGCACATGGC 120
Cy 178 ATATCTGCTGGCTGTCCAGATAATCCCTTTCAT 210
Dg 121 CAATCTGTAGTGTCTCGACGATGTTTCAT 153

RESULT 12

BM401405 542 bp mRNA linear EST 01-MAY-2002
 LOCUS GH029F Snake Bothrops insularis library IL2 Bothrops insularis cDNA
 DEFINITION 5', similar to Snake venom metalloproteinase, mRNA sequence.
 ACCESSION BM401405
 VERSION GI:20376033
 KEYWORDS EST.
 SOURCE Bothrops insularis (island jararaca)
 ORGANISM Bothrops insularis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Bothrops.
 REFERENCE 1 (bases 1 to 542)
 JOURNAL Juncqueira-de-Azevedo, I.L.M. and Ho, P.L.
 MEDLINE A survey of gene expression and diversity in the venom glands of
 PUBMED the pitviper snake Bothrops insularis through the generation of
 expressed sequence tags (ESTs)
 Gene 299 (1-2), 279-291 (2002)
 22347338
 12459276
 CONTACT: Paulo Lee Ho
 CENTRO de Biotecnologia
 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BTM06A (see Reference)
 Seq primer: M13F.
 Location/Qualifiers
 1..542
 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /feature_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL2"
 /note="Organ: Venom glands; Vector: pGEM11zf+; Site_1: Eco
 RI; Site_2: Not I; 5ug of mRNA from Bothrops insularis
 venom glands were primed with oligo-(dT) and reverse
 transcribed to cDNA using Superscript Plasmid System for
 cDNA Synthesis and Cloning (Life Technologies). The cDNAs
 were selected by size (350-600 pb and up 600 pb) in
 agarose gel electrophoresis, linked to Eco RI adaptors and
 directionally cloned in pGEM11zf+ vector (Promega). ESTs
 were generated from random clones and grouped in unique
 sequences. The putative identification of each EST or
 cluster was obtained through Blast searches (e-value <
 e-05)."

ORIGIN
 Query Match 32.0%; Score 68.2; DB 4; Length 542;
 Best Local Similarity 69.9%; Pred. No. 4.5e-10;
 Matches 107; Conservative 0; Mismatches 43; Indels 3; Gaps 1;
 Oy 61 CTGAGACGAGGGGGCAGTGTGCAAGAGGACTGTGTGACGAGATTATGAAA 120
 Db 1 CTGAATATAGGGTCACTGTGACATGAGACTGTGTGACATCAATTTAGCAA 60
 Oy 121 GAAGAACAAATATGCCGATGCGAAGGGGTGA--TGAATGATGATTACTGCATGCG 177
 Db 61 TCAGGAACAGATGCGGGGCAATGATGATGATGACCGGCTGAACACTGCACTGGC 120
 Oy 178 ATATCTGCTGCTGCTGCCAGAAATCCCTTCAT 210
 Db 121 CAATCTCTGAGTGTCTGCAAGATGCTTCAT 153

RESULT 13 565 bp mRNA linear EST 01-MAY-2002
 LOCUS BM401393
 DEFINITION GH016F Snake Bothrops insularis library IL2 Bothrops insularis cDNA
 5', similar to Snake venom metalloproteinase, mRNA sequence.
 ACCESSION BM401393

VERSION BM401393.1 GI:20376021
 KEYWORDS EST.
 SOURCE Bothrops insularis (island jararaca)
 ORGANISM Bothrops insularis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Bothrops.
 REFERENCE 1 (bases 1 to 565)
 JOURNAL Juncqueira-de-Azevedo, I.L.M. and Ho, P.L.
 MEDLINE A survey of gene expression and diversity in the venom glands of
 PUBMED the pitviper snake Bothrops insularis through the generation of
 expressed sequence tags (ESTs)
 Gene 299 (1-2), 279-291 (2002)
 22347338
 12459276
 CONTACT: Paulo Lee Ho
 CENTRO de Biotecnologia
 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BTM06A (see Reference)
 Seq primer: M13F.
 Location/Qualifiers
 1..565
 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /feature_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL2"
 /note="Organ: Venom glands; Vector: pGEM11zf+; Site_1: Eco
 RI; Site_2: Not I; 5ug of mRNA from Bothrops insularis
 venom glands were primed with oligo-(dT) and reverse
 transcribed to cDNA using Superscript Plasmid System for
 cDNA Synthesis and Cloning (Life Technologies). The cDNAs
 were selected by size (350-600 pb and up 600 pb) in
 agarose gel electrophoresis, linked to Eco RI adaptors and
 directionally cloned in pGEM11zf+ vector (Promega). ESTs
 were generated from random clones and grouped in unique
 sequences. The putative identification of each EST or
 cluster was obtained through Blast searches (e-value <
 e-05)."

ORIGIN
 Query Match 32.0%; Score 68.2; DB 4; Length 565;
 Best Local Similarity 69.9%; Pred. No. 4.5e-10;
 Matches 107; Conservative 0; Mismatches 43; Indels 3; Gaps 1;
 Oy 61 CTGAGACGAGGGGGCAGTGTGCAAGAGGACTGTGTGACGAGATTATGAAA 120
 Db 1 CTGAATATAGGGTCACTGTGACATGAGACTGTGTGACATCAATTTAGCAA 60
 Oy 121 GAAGAACAAATATGCCGATGCGAAGGGGTGA--TGAATGATGATTACTGCATGCG 177
 Db 61 TCAGGAACAGATGCGGGGCAATGATGATGATGACCGGCTGAACACTGCACTGGC 120
 Oy 178 ATATCTGCTGCTGCTGCCAGAAATCCCTTCAT 210
 Db 121 CAATCTCTGAGTGTCTGCAAGATGCTTCAT 153

RESULT 14 845 bp mRNA linear EST 27-AUG-2003
 LOCUS CF377167
 DEFINITION AGENCOURT_15341148 NICHD_XC_Swain Xenopus tropicalis cDNA clone
 IMAGE:7004048 5', mRNA sequence.
 ACCESSION CF377167
 VERSION GI:34314611
 KEYWORDS EST.
 SOURCE Xenopus tropicalis (western clawed frog)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2004, 21:14:23 ; Search time 51 Seconds

(without alignments)
137.722 Million cell updates/sec

Title: US-10-089-473a-1

Perfect score: 433
Sequence: 1 EAGEECDCGAPANPCDDAAT.....DMDYNGISAGCPRNPFNA 73

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

PIR_79:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	409	94.5	73	2	A59410 platelet aggregati
2	400	92.4	71	2	A59409 platelet-aggregati
3	400	92.4	71	2	A59411 platelet-aggregati
4	392.5	90.6	71	2	A33990 apblaggin - easter
5	391	90.3	73	2	A23731 albolabrin - green
6	391	90.3	73	2	E35982 trigramin gamma -
7	386	89.1	480	1	A30065 metalloproteinase
8	383.5	88.6	484	2	UC8020 trigramin beta-2 -
9	379	87.5	73	2	D35982 platelet aggregati
10	356	82.2	72	2	B43020 platelet aggregati
11	355	82.0	72	2	I43019 platelet aggregati
12	350	80.8	73	2	E43019 platelet aggregati
13	348	80.4	71	2	G43019 platelet aggregati
14	347	80.1	73	2	B40003 platelet aggregati
15	344	79.4	73	2	A43020 platelet aggregati
16	344	79.4	72	2	H43019 platelet aggregati
17	343	79.2	73	2	F43019 platelet aggregati
18	343	79.2	73	2	C43019 platelet aggregati
19	341	78.8	73	2	A43019 platelet aggregati
20	339	78.3	71	2	A59412 KGD-bearing plate
21	339	78.3	73	2	A40003 platelet aggregati
22	335	77.4	72	2	B43019 platelet aggregati
23	335	77.4	72	2	D43019 platelet aggregati
24	335	77.4	72	2	S43125 trilmucin precursor
25	331	76.9	71	2	A59413 platelet-aggregati
26	331	76.4	71	2	A33168 batroxastatin - ba
27	325	75.1	481	2	UC4342 fibrinolytic prote
28	316	73.0	70	2	A58649 flavonidin (valida
29	304	70.2	478	2	UC1301 hemorrhagic protei

30	293	67.7	478	2	A43296 atrolysin E (EC 3.
31	281	64.9	75	2	UX0169 cytoxic factor I
32	277.5	64.1	83	2	F35982 bitan alpha - puf
33	273	63.0	616	2	A55796 ecarin precursor -
34	269.5	62.2	83	2	A34156 bitistatin - puff
35	256	59.1	610	2	UC7530 vascular apoptosis
36	254	58.7	429	2	A42972 coagulation factor
37	251	58.0	610	2	JC6056 halyase - Gloydiu
38	237	54.7	571	2	S24789 jatarragin C, precu
39	237	54.7	609	2	SS5270 catrocollastatin p
40	234	54.0	209	2	UX0266 platelet aggregati
41	234	54.0	419	2	A59414 metalloproteinase
42	232	53.6	419	2	S41607 atrolysin A (EC 3.
43	232	53.6	478	2	UC4880 atrolysin A (EC 3.
44	231	53.3	416	2	A37877 fibrinolytic protei
45	228.5	52.8	735	2	G02937 hemorrhagic protei
					fertilin beta - cr

ALIGNMENTS

RESULT 1

A59410

platelet aggregation disintegrin (brevicaudin) 1b, venom - Gloydius haly brevicaudus

C/Species: Gloydius haly brevicaudus

C/Date: 01-Mar-2002 #sequence_revision 01-Mar-2002 #text_change 09-Jul-2004

C/Accession: A59410

R/Retada, S.

Fukuroka Univ. Sci. Reports 30, 71-78, 2000

A/Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from Gloyd

A/Reference number: A59409

A/Accession: A59410

A>Status: preliminary

A/Molecule type: protein

A/Residues: 1-73 <PER>

A/Cross-references: UNIPROT:Q90220

C/Keywords: anticoagulant; integrin inhibitor; venom

Query Match

Best Local Similarity 94.5%; Score 409; DB 2; Length 73;

Best Local Similarity 91.8%; Pred. No. 3.3e-32;

Matches 67; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY

1 EAGEECDCGAPANPCDDAATCTLRGACCAEGLCCDGRFMKEGTCMARSDMDVDCN 60

DB

1 EAGEECDCGSPNPPCDATCTLRGACCAEGLCCDGRFMKEGTCMARSDMDVDCN 60

QY

61 GISAGCPRNPFNA 73

DB

61 GISAGCPRNPFNA 73

RESULT 2

A59409

platelet-aggregation disintegrin (brevicaudin) 2b, venom - Gloydius haly brevicaudus

C/Species: Gloydius haly brevicaudus

C/Date: 01-Mar-2002 #sequence_revision 01-Mar-2002 #text_change 09-Jul-2004

C/Accession: A59409

R/Retada, S.

Fukuroka Univ. Sci. Reports 30, 71-78, 2000

A/Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from Gloyd

A/Reference number: A59409

A/Accession: A59409

A>Status: preliminary

A/Molecule type: protein

A/Residues: 1-71 <PER>

A/Cross-references: UNIPROT:Q90WC0

C/Keywords: anticoagulant; integrin inhibitor; venom

Query Match

Best Local Similarity 92.4%; Score 400; DB 2; Length 71;

Best Local Similarity 93.0%; Pred. No. 2.3e-31;

Matches 66; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY

3 GEECDGAPANPCDDAATCTLRGACCAEGLCCDGRFMKEGTCMARSDMDVDCN 62

Db 1 GEECCGSPNPGCCDAATCKLRGAGCAEGLCCDQCFMKKGTICRRARAGDDLDYCN 60
QY 63 SAGCPRNPFA 73
Db 61 SAGCPRNPFA 71

RESULT 3

A5941
platelet-aggregation disintegrin (previcaudin) 1a - Gloydus halys brevicaudus
C/Species: Gloydus halys brevicaudus
C/Date: 01-Mar-2002 #sequence_revision 01-Mar-2002 #text_change 09-Jul-2004
C/Accession: A59411
R/terada, S.
Fukuoka Univ. Sci. Reports 30, 71-78, 2000
A/Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from Gloydus
A/Reference number: A59409
A/Accession: A59411
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-71 <TER>
A/Cross-references: UNIPROT:Q90220
C/Keywords: anticoagulant; integrin inhibitor; venom

Query Match 92.4%; Score 400; DB 2; Length 71;
Best Local Similarity 91.5%; Pred. No. 2.3e-31;
Matches 65; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GEECCGAPNPGCCDAATCKLRGAGCAEGLCCDQCFMKKGTICRRARAGDDLDYCN 62
Db 1 GEECCGSPNPGCCDAATCKLRGAGCAEGLCCDQCFMKKGTICRRARAGDDLDYCN 60

QY 63 SAGCPRNPFA 73
Db 61 SAGCPRNPFA 71

RESULT 4

A3390
aplaggin - eastern cottonmouth
C/Species: Agkistrodon piscivorus piscivorus (eastern cottonmouth)
C/Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 09-Jul-2004
C/Accession: A3390
R/Chao, B.H.; Jakubowski, J.A.; Savage, B.; Chou, E.P.; Marzoc, U.M.; Harper, L.A.; Mara
Proc. Natl. Acad. Sci. U.S.A. 86, 8050-8054, 1989
A/Title: Agkistrodon piscivorus piscivorus platelet aggregation inhibitor: a potent inhibi
A/Reference number: A33900; MUID:90046735; PMID:2510158
A/Accession: A33900
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-71 <CHA>
A/Cross-references: UNIPROT:P16338
C/Superfamily: unassigned disintegrins; disintegrin homology
F/1-68/Domain: disintegrin homology (fragment) <DIS>

Query Match 90.6%; Score 392.5; DB 2; Length 71;
Best Local Similarity 90.3%; Pred. No. 1.2e-30;
Matches 65; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 EAGEBCDGGAPNPGCCDAATCKLRGAGCAEGLCCDQCFMKKGTICRRARAGDDLDYCN 60
Db 1 EAGEBCDGGSPNPGCCDAATCKLRGAGCAEGLCCDQCFMKKGTICRRARAGDDLDYCN 59

QY 61 GISAGCPRNPFA 72
Db 60 GISAGCPRNPFA 71

RESULT 5

A23731
albolabrin - green pit viper
C/Species: Trimereurus albolabris (green pit viper)

C/Date: 28-Feb-1992 #sequence_revision 23-Aug-1997 #text_change 09-Jul-2004
C/Accession: A23731; S43021
R/Calvete, J.J.; Schaefer, W.; Soszka, T.; Lu, W.; Cook, J.J.; Jameson, B.A.; Niewiarow
Biochemistry 30, 5225-5229, 1991
A/Title: Identification of the disulfide bond pattern in albolabrin, an RGD-containing
itory activity.
A/Reference number: A23731; MUID:91242430; PMID:2036389

A/Accession: A23731
A/Molecule type: protein
A/Residues: 1-73 <CAL>
A/Cross-references: UNIPROT:P17496
R/Asajima, M.; Smith, K.J.; Lu, X.; Williams, J.A.; Trayer, H.; Trayer, I.P.; Hyde, E.L.
Bull. J. Biochem 218, 853-860, 1993
A/Title: (1)H-NMR studies and secondary structure of the RGD-containing snake toxin, al
A/Reference number: S43021; MUID:94105384; PMID:8281937
A/Accession: S43021
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-73 <JAS>

C/Function: inhibits cell adhesion and platelet aggregation
A/Description: inhibits cell adhesion and platelet aggregation
C/Superfamily: unassigned disintegrins; disintegrin homology
C/Keywords: venom
F/1-65/Domain: disintegrin homology (fragment) <DIS>
F/51-53/Region: cell attachment (R-G-D) motif
F/29-59,47-66/Disulfide bonds: #status experimental

Query Match 90.3%; Score 391; DB 2; Length 73;
Best Local Similarity 87.7%; Pred. No. 1.6e-30;
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPNPGCCDAATCKLRGAGCAEGLCCDQCFMKKGTICRRARAGDDLDYCN 60
Db 1 EAGEBCDGGSPNPGCCDAATCKLRGAGCAEGLCCDQCFMKKGTICRRARAGDDLDYCN 60

QY 61 GISAGCPRNPFA 73
Db 61 GISAGCPRNPFA 73

RESULT 6

E35982
trigemin gamma - Indian green tree viper
C/Species: Trimereurus gramineus (Indian green tree viper)
C/Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 16-Aug-2004
C/Accession: E35982
R/Dennis, M.S.; Henzel, W.J.; Pitti, R.M.; Lipari, M.T.; Napier, M.A.; Delcher, T.A.; Bu
Proc. Natl. Acad. Sci. U.S.A. 87, 2471-2475, 1990
A/Title: Platelet glycoprotein IIb-IIIa protein antagonists from snake venoms: evidence
A/Reference number: A35982; MUID:90207217; PMID:2320569
A/Accession: E35982
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-73 <DEN>
A/Cross-references: UNIPROT:P17496
C/Superfamily: disintegrin homology (fragment) <DIS>
F/1-69/Domain: disintegrin homology (fragment) <DIS>
F/51-53/Region: cell attachment (R-G-D) motif

Query Match 90.3%; Score 391; DB 2; Length 73;
Best Local Similarity 87.7%; Pred. No. 1.6e-30;
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPNPGCCDAATCKLRGAGCAEGLCCDQCFMKKGTICRRARAGDDLDYCN 60
Db 1 EAGEBCDGGSPNPGCCDAATCKLRGAGCAEGLCCDQCFMKKGTICRRARAGDDLDYCN 60

QY 61 GISAGCPRNPFA 73
Db 61 GISAGCPRNPFA 73

RESULT 7

A30065
trigramin precursor - Indian green tree viper
N/Contains: hemorrhetic proteinase (EC 3.4.24.-); platelet aggregation inhibitor (disint
C/Species: Trimeresurus gramineus (Indian green tree viper)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
A/Accession: S12589; A30065; A29784
R/Neper, M.P.; Jacobson, M.A.
Nucleic Acids Res. 18, 4255, 1990
A/Title: Sequence of a cDNA encoding the platelet aggregation inhibitor trigramin.
A/Reference number: S12589; MUID:90332429; PMID:2377470
A/Accession: S12589
A/Molecule type: mRNA
A/Residues: 1-480 <NDB>
A/Cross-references: UNIPROT:P15503; EMBL:X51530; NID:964407; PIDN:CA35910.1; PID:964408
A/Note: translation of the signal sequence and the mature protein but not of the propept
R/Huang, T.F.; Holt, J.C.; Kizdy, E.F.; Niewiarowski, S.
Biochemistry 28, 661-666, 1989
A/Title: Trigramin: primary structure and its inhibition of von Willebrand factor bindin
A/Reference number: A30065; MUID:89229063; PMID:2653425
A/Accession: A30065
A/Molecule type: protein
A/Residues: 408-479 <HUA>
R/Huang, T.F.; Holt, J.C.; Lukaeiwicz, H.; Niewiarowski, S.
J. Biol. Chem. 262, 16157-16163, 1987
A/Title: Trigramin, A low molecular weight peptide inhibiting fibrinogen interaction with
A/Reference number: A29784; MUID:88058981; PMID:3680247
A/Accession: A29784
A/Molecule type: protein
A/Residues: 408-419 <HUN>
C/Superfamily: trigramin precursor, disintegrin homology
C/Keywords: anticoagulant; glycoprotein; hydrolase; metalloproteinase; venom; zinc; zymo
F/1-18/Domain: signal sequence #status predicted <SIG>
F/398-476/Domain: disintegrin homology <DIS>
F/408-479/Product: trigramin #status experimental <MAT>
F/458-460/Region: cell attachment (R-G-D) motif
F/427/Binding site: carbohydrate (asn) (covalent) #status predicted
F/333,337,343/Binding site: zinc (His) #status predicted
F/334/Active site: Glu #status predicted

Query Match 89.1%; Score 386; DB 1; Length 480;
Best Local Similarity 84.9%; Pred. No. 1.9e-29;
Matches 62; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAGEECDCGAPNPPCCDAATCTKLRPGACAGLCCDDGCFMKEGTICRMARDDMDYCN 60
DB 408 EAGEECDCGSPNPPCCDAATCTKLRPGACGGLCCDDGCFIEGTICRIARDDLDYCN 467

QY 61 GISAGCPRNPFA 73
DB 468 GRSAGCPRNPFA 480

RESULT 8
JC8020
metalloproteinase-disintegrin protein, Jerdonitn - Trimeresurus jerdoni
C/Species: Trimeresurus jerdoni
C/Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004
A/Accession: JC8020; PC7231
R/Chen, R.Q.; Jin, Y.; Wu, J.B.; Zhou, X.D.; Lu, Q.M.; Wang, W.Y.; Xiong, Y.L.
Biochem. Biophys. Res. Commun. 310, 182-187, 2003
A/Title: A new protein structure of P-II class snake venom metalloproteinases: It compl
A/Reference number: JC8020; PMID: 14511668
A/Accession: JC8020
A/Molecule type: mRNA
A/Residues: 1-484 <CHE>
A/Cross-references: GB:AY364231
A/Experimental source: Crude venom
A/Accession: PC7231
A/Molecule type: protein
A/Residues: 206-214;221-233;239-308;310-344;451-453;460-484 <CH2>
A/Comment: This protein, a new metalloproteinase-disintegrin protein, belongs to the cla
sion with IC50 of 120nM.
C/Keywords: Jerdonitn; metalloproteinase-disintegrin; platelet aggregation; SWP

Query Match 88.6%; Score 383.5; DB 2; Length 484;
Best Local Similarity 82.9%; Pred. No. 3.3e-29;
Matches 63; Conservative 7; Mismatches 3; Indels 3; Gaps 1;

QY 1 EAGEECDCGAPNPPCCDAATCTKLRPGACAGLCCDDGCFMKEGTICRMARDDMDY 57
DB 409 EVGEEDDCGSPNPPCCDAATCTKLRPGACGGLCCDDGCFMKEGTICRIARDDLD 468

QY 58 YNGISAGCPRNPFA 73
DB 469 YNGISAGCPRNPFA 484

RESULT 9
D35982
trigramin beta-2 - Indian green tree viper
N/Contains: trigramin beta-1
C/Species: Trimeresurus gramineus (Indian green tree viper)
C/Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 16-Aug-2004
A/Accession: D35982; C35982
R/Dennis, M.S.; Hentzel, W.J.; Pitti, R.M.; Lipari, M.T.; Napier, M.A.; Deisher, T.A.; B
Proc. Natl. Acad. Sci. U.S.A. 87, 2471-2475, 1990
A/Title: Platelet glycoprotein IIb-IIIa protein antagonists from snake venoms: evidence
A/Reference number: A35982; MUID:90207217; PMID:2320569
A/Accession: D35982
A/Molecule type: protein
A/Residues: 1-73 <DEN>
A/Cross-references: UNIPROT:P17495
A/Accession: C35982
A/Molecule type: protein
A/Residues: 1-72 <DE2>
C/Superfamily: disintegrin homology
C/Keywords: Venom
F/1-73/Product: trigramin beta-2 #status experimental <MA2>
F/1-72/Product: trigramin beta-1 #status experimental <MA1>
F/1-72/Domain: disintegrin homology (fragment) <DIS>
F/51-53/Region: cell attachment (R-G-D) motif

Query Match 87.5%; Score 379; DB 2; Length 73;
Best Local Similarity 84.9%; Pred. No. 2.3e-29;
Matches 62; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EAGEECDCGAPNPPCCDAATCTKLRPGACAGLCCDDGCFMKEGTICRMARDDMDYCN 60
DB 1 EAGKDDCGSPNPPCCDAATCTKLRPGACGGLCCDDGCFMKEGTICRIARDDLDYCN 60

QY 61 GISAGCPRNPFA 73
DB 61 GRSAGCPRNPFA 73

RESULT 10
B43020
platelet aggregation disintegrin (cereberin), venom - Arizona black rattlesnake
C/Species: Crotalus viridis cerberus (Arizona black rattlesnake)
C/Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
A/Accession: B43020
R/Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten,
J. Biol. Chem. 268, 1058-1065, 1993
A/Title: Characterization of the integrin specificities of disintegrins isolated from A
A/Reference number: A43019; MUID:93123215; PMID:8419314
A/Accession: B43020
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-72 <SCA>
A/Cross-references: UNIPROT:P1985
C/Superfamily: unassigned disintegrins; disintegrin homology
F/3-69/Domain: disintegrin homology <DIS>

Query Match 82.2%; Score 356; DB 2; Length 72;
Best Local Similarity 83.3%; Pred. No. 3.4e-27;
Matches 60; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

A:Molecule type: protein
 A:Residues: 1-73 <SCA>
 C:Superfamily: unassigned disintegrins; disintegrin homology
 F:3-69/Domain: disintegrin homology <DIS>

Query Match 79.4%; Score 344; DB 2; Length 73;
 Best Local Similarity 80.8%; Pred. No. 4.6e-26;
 Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY	1	EAGEECDCGAPNCCDAATCKLRPGAQCAEGLCDDOCRFMKEGTICRMARGDDMDPYCN	60
Db	1	EAGEECDCGTRGNPCDDAATCKLRPGAQCAEGLCDDOCRFMKAGKICRRARGDNPDDRCT	60
QY	61	GISAGCPNNPFA	73
Db	61	QGSADCPNNRFA	73

Search completed: December 3, 2004, 21:39:13
 Job time : 51 secs

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OM protein - protein search, using sw model

Run on: December 3, 2004, 21:26:53 / Search time 53 Seconds
(without alignments)
91.344 Million cell updates/sec

Title: US-10-089-473a-1

Perfect score: 433 EAGEBCDCGAPNPPCDAT.....DMDYCNISAGCPNPFH 73

Sequence: 1

Scoring table: BLOSUM62

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	402	92.8	72 6 5182260-21	Patent No. 5182260
2	402	92.8	73 6 5182260-2	Patent No. 5182260
3	395	91.2	73 4 US-05-776-268A-1	Sequence 1, Appl1
4	392.5	90.6	71 1 US-07-965-674-10	Sequence 10, Appl1
5	392.5	90.6	71 4 US-09-460-295B-7	Sequence 7, Appl1
6	392.5	90.6	71 5 PCT-US93-09523-10	Sequence 10, Appl1
7	391	90.3	73 1 US-07-965-674-14	Sequence 14, Appl1
8	391	90.3	73 3 US-08-993-165-15	Sequence 15, Appl1
9	391	90.3	73 4 US-08-243-640-13	Sequence 13, Appl1
10	391	90.3	73 4 US-08-929-847-15	Sequence 15, Appl1
11	391	90.3	73 4 US-09-460-295B-9	Sequence 9, Appl1
12	391	90.3	73 4 US-09-813-484-15	Sequence 15, Appl1
13	391	90.3	73 5 PCT-US93-09523-14	Sequence 14, Appl1
14	390	90.1	99 1 US-07-623-611-5	Sequence 5, Appl1
15	390	90.1	99 1 US-07-623-611-8	Sequence 8, Appl1
16	390	90.1	99 5 PCT-US91-09108-5	Sequence 5, Appl1
17	390	90.1	99 5 PCT-US91-09108-8	Sequence 8, Appl1
18	390	90.1	106 1 US-07-623-611-4	Sequence 4, Appl1
19	390	90.1	106 1 US-07-623-611-7	Sequence 7, Appl1
20	390	90.1	106 5 PCT-US91-09108-4	Sequence 4, Appl1
21	390	90.1	106 5 PCT-US91-09108-7	Sequence 7, Appl1
22	387	89.4	98 1 US-07-623-611-6	Sequence 6, Appl1
23	387	89.4	98 1 US-07-623-611-9	Sequence 9, Appl1
24	387	89.4	98 5 PCT-US91-09108-6	Sequence 6, Appl1
25	387	89.4	98 5 PCT-US91-09108-9	Sequence 9, Appl1
26	386	89.1	73 4 US-09-540-448-15	Sequence 15, Appl1
27	386	89.1	552 4 US-09-460-295B-8	Sequence 8, Appl1

28	384.5	88.8	71 1 US-07-602-847C-24	Sequence 24, Appl1
29	384	88.7	72 1 US-07-623-611-1	Sequence 1, Appl1
30	384	88.7	72 5 PCT-US91-09108-1	Sequence 1, Appl1
31	384	88.7	96 1 US-07-623-611-2	Sequence 2, Appl1
32	384	88.7	96 1 US-07-623-611-3	Sequence 3, Appl1
33	384	88.7	96 5 PCT-US91-09108-2	Sequence 2, Appl1
34	384	88.7	96 5 PCT-US91-09108-3	Sequence 3, Appl1
35	382	88.2	72 1 US-07-602-847C-23	Sequence 23, Appl1
36	371.5	85.8	73 1 US-07-965-674-5	Sequence 5, Appl1
37	371.5	85.8	73 5 PCT-US93-09523-5	Sequence 5, Appl1
38	368	85.0	483 4 US-09-460-295B-2	Sequence 2, Appl1
39	350	80.4	73 6 518899-6	Patent No. 518899
40	348	80.4	71 6 518899-11	Patent No. 518899
41	347	80.1	73 6 518899-3	Patent No. 518899
42	344	79.4	73 6 518899-2	Patent No. 518899
43	341.5	78.9	71 6 518899-13	Patent No. 518899
44	341	78.8	72 6 518899-9	Patent No. 518899
45	341	78.8	73 6 518899-4	Patent No. 518899

ALIGNMENTS

RESULT 1
5182260-21
; Patent No. 5182260
; APPLICANT: MARAGANORE, JOHN M., JAKUBOWSKI, JOSEPH A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
; THOSE INHIBITORS AND COMPOSITIONS USING THEM
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,313
; FILING DATE: 01-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 303,585
; FILING DATE: 27-JAN-1989
; APPLICATION NUMBER: 303,590
; FILING DATE: 27-JAN-1989
; SEQ ID NO:21:
; LENGTH: 72
5182260-21.

Query Match 92.8%; Score 402; DB 6; Length 72;
Best Local Similarity 90.3%; Pred. No. 1.6e-30;
Matches 65; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAGEBCDCGAPNPPCDATCKLRGACACAGELCCDCCRFMKEGTICRMARGDMDYCN 60
DB 1 EAGEBCDCGSPNPPCDATCKLRGACACAGELCCDCKFMKEGTVCRARDDVDYCN 60
QY 61 GISAGCPNPFH 72
DB 61 GISAGCPNPFH 72
RESULT 2
5182260-2
; Patent No. 5182260
; APPLICANT: MARAGANORE, JOHN M., JAKUBOWSKI, JOSEPH A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
; THOSE INHIBITORS AND COMPOSITIONS USING THEM
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,313
; FILING DATE: 01-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 303,585
; FILING DATE: 27-JAN-1989
; APPLICATION NUMBER: 303,590
; FILING DATE: 27-JAN-1989
; SEQ ID NO:2:

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LENGTH: 73
5182260-2

Query Match          92.8%; Score 402; DB 6; Length 73;
Best Local Similarity 90.3%; Pred. No. 1.6e-30;
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QY 1 EAGEBCDGGAPANPCDDATCTLRPGACAGLCCDCCRFMKEGTICRMARGDDMDYCN 60
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DB 2 EAGEBCDGGSPENPCDDATCTLRPGACAGLCCDCCRFMKEGTICRMARGDDMDYCN 61

QY 61 GISACCPNPFH 72
   |||||
DB 62 GISACCPNPFH 73

RESULT 3
US-09-776-268A-1
; Sequence 1, Application US/09776268A
; Patent No. 6537551
; GENERAL INFORMATION:
; APPLICANT: KIM, DOO-SIK
; APPLICANT: CHUNG, KWANG HOE
; APPLICANT: KANG, JIN-CHEOL
; TITLE OF INVENTION: ANTI-TUMOR AGENT COMPRISING SALMOSIN AS AN ACTIVE INGREDIENT
; FILE REFERENCE: 0136/1F733-US1
; CURRENT APPLICATION NUMBER: US/09/776,268A
; PRIOR FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: US 09/335,088
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: KR 99-20579
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: KR 98-23778
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Agkistrodon halys brevicaudus
US-09-776-268A-1

Query Match          91.2%; Score 395; DB 4; Length 73;
Best Local Similarity 90.4%; Pred. No. 7.1e-30;
Matches 66; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPANPCDDATCTLRPGACAGLCCDCCRFMKEGTICRMARGDDMDYCN 60
   |||||
DB 1 EAGEBCDGGSPENPCDDATCTLRPGACAGLCCDCCRFMKEGTICRMARGDDMDYCN 60

QY 61 GISACCPNPFH 73
   |||||
DB 61 GISACCPNPFH 73

RESULT 4
US-07-965-674-10
; Sequence 10, Application US/07965674
; Patent No. 5380646
; GENERAL INFORMATION:
; APPLICANT: Knight, Linda C.
; TITLE OF INVENTION: Thrombus Detection Using
; TITLE OF INVENTION: Radio-labelled Disintegrins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Temple University - Of The Common-
; ADDRESSEE: wealth System of Higher Education
; STREET: 406 University Services Building
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19122
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/965,674
FILING DATE: 19921019
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-173
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-5549
TELEFAX: (215) 568-8383
TELEX: No. 5380646e
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-965-674-10

Query Match          90.6%; Score 392.5; DB 1; Length 71;
Best Local Similarity 90.3%; Pred. No. 1.2e-29;
Matches 65; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 EAGEBCDGGAPANPCDDATCTLRPGACAGLCCDCCRFMKEGTICRMARGDDMDYCN 60
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DB 1 EAGEBCDGGSPENPCDDATCTLRPGACAGLCCDCCRFMKEGTICRMARGDDMDYCN 59

QY 61 GISACCPNPFH 72
   |||||
DB 60 GISACCPNPFH 71

RESULT 5
US-09-460-295B-7
; Sequence 7, Application US/09460295B
; Patent No. 6710030
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; TITLE OF INVENTION: COMFORTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
; FILE REFERENCE: 1279-338C3/09801388
; CURRENT APPLICATION NUMBER: US/09/460,295B
; PRIOR FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: US 09/163,047
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Agkistrodon piscivorus
US-09-460-295B-7

Query Match          90.6%; Score 392.5; DB 4; Length 71;
Best Local Similarity 90.3%; Pred. No. 1.2e-29;
Matches 65; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 EAGEBCDGGAPANPCDDATCTLRPGACAGLCCDCCRFMKEGTICRMARGDDMDYCN 60
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DB 1 EAGEBCDGGSPENPCDDATCTLRPGACAGLCCDCCRFMKEGTICRMARGDDMDYCN 59

QY 61 GISACCPNPFH 72
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DB 60 GISACCPNPFH 71
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RESULT 6
PCT-US93-09523-10
Sequence 10, Application PC/TUS9309523
GENERAL INFORMATION:
APPLICANT: Temple University - Of The Commonwealth
APPLICANT: System of Higher Education
APPLICANT: Knight, Linda C. and
APPLICANT: Maurer, Alan H.
TITLE OF INVENTION: Thrombus Detection Using
TITLE OF INVENTION: Radiolabelled Disintegrins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Temple University - Of The
STREET: 406 University Services Building
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19122
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09523
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 965,674
FILING DATE: 19 October 1992
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-173 PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8363
TELEFAX: (215) 568-5549
TELEX: None
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-09523-10

Query Match 90.6%; Score 392.5; DB 5; Length 71;
Best Local Similarity 90.3%; Pred. No. 1.2e-29;
Matches 65; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 EAGEECCGAPANPCDDATCKLRPGAQCAEGLCDDCFMKKEGTTICRMARGDDMDYCN 60
DB 1 EAGEECCGSPENPCDDATCKLRPGAQCAEGLCDDCFMKKEGTTICRMARGDDMDYCN 59

QY 61 GISAGCPRNPFH 72
DB 60 GISAGCPRNPFH 71

RESULT 7
US-07-965-674-14
Sequence 14, Application US/07965674
Patent No. 5380646
GENERAL INFORMATION:
APPLICANT: Knight, Linda C.
TITLE OF INVENTION: Thrombus Detection Using
TITLE OF INVENTION: Radiolabelled Disintegrins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Temple University - Of The Common-
STREET: wealth System of Higher Education
STREET: 406 University Services Building
CITY: Philadelphia

STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19122
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/965,674
FILING DATE: 19921019
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-173
TELEPHONE: (215) 568-8363
TELEFAX: (215) 568-5549
TELEX: No. 5380646e
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-965-674-14

Query Match 90.3%; Score 391; DB 1; Length 73;
Best Local Similarity 87.7%; Pred. No. 1.6e-29;
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEECCGAPANPCDDATCKLRPGAQCAEGLCDDCFMKKEGTTICRMARGDDMDYCN 60
DB 1 EAGEECCGSPANPCDDATCKLRPGAQCAEGLCDDCFMKKEGTTICRMARGDDMDYCN 60

QY 61 GISAGCPRNPFH 73
DB 61 GISAGCPRNPFH 73

RESULT 8
US-08-993-165-15
Sequence 15, Application US/08993165A
Patent No. 6123923
GENERAL INFORMATION:
APPLICANT: Unger, Evan C
APPLICANT: Wu, Yungliu
TITLE OF INVENTION: Optoacoustic Contrast Agents And Methods For Their Use
FILE REFERENCE: UNGR1224
CURRENT APPLICATION NUMBER: US/08/993,165A
CURRENT FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 15
LENGTH: 73
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. 6123923e1 Sequence
US-08-993-165-15

Query Match 90.3%; Score 391; DB 3; Length 73;
Best Local Similarity 87.7%; Pred. No. 1.6e-29;
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEECCGAPANPCDDATCKLRPGAQCAEGLCDDCFMKKEGTTICRMARGDDMDYCN 60
DB 1 EAGEECCGSPANPCDDATCKLRPGAQCAEGLCDDCFMKKEGTTICRMARGDDMDYCN 60

QY 61 GISAGCPRNPFH 73

Db 61 GISAGCPNPLHA 73

RESULT 9

US-09-243-640-13

Sequence 13, Application US/09243640

Patent No. 6521211

GENERAL INFORMATION:

APPLICANT: Unger, Evan C

APPLICANT: Shen, Dekang

APPLICANT: Wu, Guanli

TITLE OF INVENTION: No. 6521211el Methods Of Imaging And Treatment With Targeted

FILE REFERENCE: DUP-0463

CURRENT APPLICATION NUMBER: US/09/243,640

PRIOR FILING DATE: 1999-02-03

PRIOR APPLICATION NUMBER: 08/660,032

PRIOR FILING DATE: 1996-06-06

PRIOR APPLICATION NUMBER: 08/640,464

PRIOR FILING DATE: 1996-05-01

PRIOR APPLICATION NUMBER: 08/497,684

PRIOR FILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: 09/218,660

PRIOR FILING DATE: 1998-12-22

PRIOR APPLICATION NUMBER: 60/073,913

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentln Ver. 2.1

SEQ ID NO 13

LENGTH: 73

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: No. 6521211el Sequence

US-09-243-640-13

Query Match

Best Local Similarity 90.3%; Score 391; DB 4; Length 73;

Best Local Similarity 87.7%; Pred. No. 1.6e-29;

Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPNPPCCDAATCKLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 60

Db 1 EAGEBCDGGAPNPPCCDAATCKLRPGAQCGEGLCCDQCFMKKGITCRARAGDDLDYCN 60

QY 61 GISAGCPNPLHA 73

Db 61 GISAGCPNPLHA 73

RESULT 10

US-08-929-847-15

Sequence 15, Application US/08929847

Patent No. 6548047

GENERAL INFORMATION:

APPLICANT: Unger, Evan C.

TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled Compositions

FILE REFERENCE: BMS0441

CURRENT APPLICATION NUMBER: US/08/929,847

PRIOR FILING DATE: 1997-09-15

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentln version 3.1

SEQ ID NO 15

LENGTH: 73

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Completely synthetic sequence

US-08-929-847-15

Query Match

Best Local Similarity 90.3%; Score 391; DB 4; Length 73;

Best Local Similarity 87.7%; Pred. No. 1.6e-29;

Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPNPPCCDAATCKLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 60

Db 1 EAGEBCDGGAPNPPCCDAATCKLRPGAQCGEGLCCDQCFMKKGITCRARAGDDLDYCN 60

QY 61 GISAGCPNPLHA 73

Db 61 GISAGCPNPLHA 73

RESULT 11

US-09-460-295B-9

Sequence 9, Application US/09460295B

Patent No. 6710030

GENERAL INFORMATION:

APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA

TITLE OF INVENTION: CONTRASTOSTATION (CN) AND METHODS FOR ITS USE IN PREVENTING METAS

FILE REFERENCE: 1279-338C3/09801388

CURRENT APPLICATION NUMBER: US/09/460,295B

PRIOR FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: US 09/163,047

PRIOR FILING DATE: 1998-09-29

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentln version 3.1

SEQ ID NO 9

LENGTH: 73

TYPE: PRT

ORGANISM: Trimeresurus abalabris

US-09-460-295B-9

Query Match

Best Local Similarity 90.3%; Score 391; DB 4; Length 73;

Best Local Similarity 87.7%; Pred. No. 1.6e-29;

Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPNPPCCDAATCKLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 60

Db 1 EAGEBCDGGAPNPPCCDAATCKLRPGAQCGEGLCCDQCFMKKGITCRARAGDDLDYCN 60

QY 61 GISAGCPNPLHA 73

Db 61 GISAGCPNPLHA 73

RESULT 12

US-09-813-484-15

Sequence 15, Application US/09813484

Patent No. 6716412

GENERAL INFORMATION:

APPLICANT: Unger, Evan C.

TITLE OF INVENTION: No. 6716412el Methods Of Ultrasound Treatment Using Gas Or Gaseo

FILE REFERENCE: UNGR1600

CURRENT APPLICATION NUMBER: US/09/813,484

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 08/929,847

PRIOR FILING DATE: 1997-09-15

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentln version 3.1

SEQ ID NO 15

LENGTH: 73

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Completely synthetic sequence

US-09-813-484-15

Query Match

Best Local Similarity 90.3%; Score 391; DB 4; Length 73;

Best Local Similarity 87.7%; Pred. No. 1.6e-29;

Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEBCDGGAPNPPCCDAATCKLRPGAQCAEGLCCDQCFMKEGTICRMARGDDMDYCN 60

Db 1 EAGEBDCGSPANPCDDATCKLRPGAQCGEGLCDDCGCFMKKGTICRRARGGDDLDYCN 60
QY 61 GISAGCPRNPFHA 73
Db 61 GISAGCPRNPLHA 73

RESULT 13

PCT-US93-09523-14
Sequence 14, Application PC/TUS9309523
GENERAL INFORMATION:
APPLICANT: Temple University - Of The Commonwealth
APPLICANT: System of Higher Education
APPLICANT: Knight, Linda C. and
APPLICANT: Maurer, Alan H.
TITLE OF INVENTION: Thrombus Detection Using
TITLE OF INVENTION: Radiolabelled Disintegrins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Temple University - Of The
ADDRESSEE: Commonwealth System of Higher Education
STREET: 406 University Services Building
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19122
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09523
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 965,674
FILING DATE: 19 October 1992
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-173 PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8363
TELEFAX: (215) 568-5549
TELEX: None
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-09523-14

Query Match 90.3%; Score 391; DB 5; Length 73;
Best Local Similarity 87.7%; Pred. No. 1.6e-29;
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGEBDCGAPANPCDDATCKLRPGAQCAAGLCCDQCFMKKEGTICRMARGDDMDYCN 60
Db 1 EAGEBDCGSPANPCDDATCKLRPGAQCGEGLCDDCGCFMKKGTICRRARGGDDLDYCN 60

QY 61 GISAGCPRNPFHA 73
Db 61 GISAGCPRNPLHA 73

RESULT 14
US-07-623-611-5
Sequence 5, Application US/07623611
Patent No. 5242810
GENERAL INFORMATION:
APPLICANT: Maraganore, John M.
APPLICANT: Chao, Betty H.

APPLICANT: Strauch, Kathryn L.
APPLICANT: Thompson, Jeffrey S.
TITLE OF INVENTION: BIFUNCTIONAL INHIBITORS OF THROMBIN AND
TITLE OF INVENTION: PLATELET ACTIVATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue - 29th Floor
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/623,611
FILING DATE: 19901207
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 715-0600
TELEFAX: (212) 715-0674
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-623-611-5

Query Match 90.1%; Score 390; DB 1; Length 99;
Best Local Similarity 88.9%; Pred. No. 2.7e-29;
Matches 64; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAGEBDCGAPANPCDDATCKLRPGAQCAAGLCCDQCFMKKEGTICRMARGDDMDYCN 60
Db 28 EAGEBDCGSPANPCDDATCKLRPGAQCAAGLCCDQCFMKKEGTICRRARGGDDVDYCN 87

QY 61 GISAGCPRNPFH 72
Db 88 GISAGCPRNPFH 99

RESULT 15

US-07-623-611-8
Sequence 8, Application US/07623611
Patent No. 5242810
GENERAL INFORMATION:
APPLICANT: Maraganore, John M.
APPLICANT: Chao, Betty H.
APPLICANT: Strauch, Kathryn L.
APPLICANT: Thompson, Jeffrey S.
TITLE OF INVENTION: BIFUNCTIONAL INHIBITORS OF THROMBIN AND
TITLE OF INVENTION: PLATELET ACTIVATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue - 29th Floor
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.24
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/623,611
 ; FILING DATE: 19901207
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Haley Jr., James F.
 ; REGISTRATION NUMBER: 27,794
 ; REFERENCE/DOCKET NUMBER: B154
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 715-0600
 ; TELEFAX: (212) 715-0674
 ; TELEX: 14-8367
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 99 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ;
 ; US-07-623-611-8

Query Match 90.1%; Score 390; DB 1; Length 99;
 Best Local Similarity 88.9%; Pred. No. 2.7e-29;
 Matches: 64; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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QY	61	GISAGCPRRNPFH	72		
DB	64	GISAGCPRRNPFH	75		

Search completed: December 3, 2004, 21:40:19
 Job time : 54 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2004, 21:38:18 (Search time 104 Seconds

(Without alignments)
250.322 Million cell updates/sec

Title: US-10-089-473a-1

Perfect score: 433

Sequence: 1 EAGEEDCDGAPNPPCCDAAT.....DMDYCNISAGCPNPFHA 73

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Gapop 10.0, Gapext 0.5

Searched: 1582122 seqs, 35623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database: Published Applications_AA:*

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20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	395	91.2	73	US-09-776-268A-1	Sequence 1, Appl1
2	392.5	90.6	71	US-09-832-501-37	Sequence 37, Appl1
3	392.5	90.6	71	US-10-439-532-7	Sequence 7, Appl1
4	392.5	90.6	71	US-10-712-584-7	Sequence 7, Appl1
5	391	90.3	73	US-09-813-484-15	Sequence 15, Appl1
6	391	90.3	73	US-10-439-532-9	Sequence 9, Appl1
7	391	90.3	73	US-10-712-584-5	Sequence 15, Appl1
8	386	89.1	73	US-10-466-801-15	Sequence 15, Appl1
9	386	89.1	552	US-10-439-532-8	Sequence 8, Appl1
10	386	89.1	552	US-10-712-584-8	Sequence 8, Appl1
11	368	85.0	483	US-10-439-532-2	Sequence 2, Appl1
12	368	85.0	483	US-10-712-584-2	Sequence 2, Appl1
13	360	83.1	478	US-10-078-866-2	Sequence 2, Appl1

14	335	77.4	463	15	US-10-383-588A-2	Sequence 2, Appl1
15	335	77.4	481	15	US-10-383-588A-8	Sequence 8, Appl1
16	333	76.9	73	14	US-10-439-532-10	Sequence 10, Appl1
17	333	76.9	73	16	US-10-712-584-10	Sequence 10, Appl1
18	326	75.3	71	15	US-10-383-588A-6	Sequence 6, Appl1
19	316	73.0	69	9	US-09-813-484-14	Sequence 14, Appl1
20	313	72.3	70	10	US-09-961-856-9	Sequence 9, Appl1
21	312.5	72.2	68	9	US-09-813-484-16	Sequence 16, Appl1
22	312.5	72.2	68	14	US-10-046-801-16	Sequence 16, Appl1
23	305	70.4	70	9	US-09-813-484-17	Sequence 17, Appl1
24	305	70.4	70	14	US-10-046-801-17	Sequence 17, Appl1
25	301	69.5	69	14	US-10-439-532-11	Sequence 11, Appl1
26	287	66.3	68	14	US-10-712-584-11	Sequence 11, Appl1
27	287	66.3	68	16	US-10-712-584-11	Sequence 11, Appl1
28	281	64.9	478	14	US-10-439-532-14	Sequence 14, Appl1
29	281	64.9	478	16	US-10-712-584-14	Sequence 14, Appl1
30	279	64.4	400	9	US-09-921-823-2	Sequence 2, Appl1
31	275	63.5	611	9	US-09-921-823-17	Sequence 17, Appl1
32	260	60.0	111	9	US-09-921-823-23	Sequence 23, Appl1
33	260	60.0	195	9	US-09-921-823-8	Sequence 8, Appl1
34	258.5	59.7	76	10	US-09-877-843-8	Sequence 8, Appl1
35	240.5	55.5	606	14	US-10-439-532-12	Sequence 12, Appl1
36	240.5	55.5	606	16	US-10-712-584-12	Sequence 12, Appl1
37	237	54.7	571	14	US-10-439-532-13	Sequence 13, Appl1
38	237	54.7	571	16	US-10-712-584-13	Sequence 13, Appl1
39	225	52.0	776	9	US-09-908-193-13	Sequence 13, Appl1
40	224	51.7	87	9	US-09-955-504-24	Sequence 24, Appl1
41	224	51.7	87	13	US-10-125-452-24	Sequence 24, Appl1
42	224	51.7	150	9	US-09-983-531A-28	Sequence 28, Appl1
43	224	51.7	394	9	US-09-983-531A-16	Sequence 16, Appl1
44	224	51.7	395	15	US-10-343-251A-45	Sequence 45, Appl1
45	224	51.7	427	9	US-09-983-531A-20	Sequence 20, Appl1

ALIGNMENTS

RESULT 1
US-09-776-268A-1
; Sequence 1, Application US/09776268A
; Publication No. US2001002342A1
; GENERAL INFORMATION:
; APPLICANT: KIM, DOO-SIK
; APPLICANT: CHUNG, Kwang Hoe
; APPLICANT: KANG, In-Cheol
; TITLE OF INVENTION: ANTI-TUMOR AGENT COMPRISING SALMOSIN AS AN ACTIVE INGREDIENT
; FILE REFERENCE: 0136/15733-US1
; CURRENT APPLICATION NUMBER: US/09/776,268A
; PRIOR FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: US 09/335,088
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: KR 99-20579
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: KR 98-23778
; PRIOR FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Agkistrodon halys brevicaudus
US-09-776-268A-1

Query Match 91.2%; Score 395; DB 9; Length 73;
Best Local Similarity 90.4%; Pred. No. 3,5e-31;
Matches 66; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Cy 1 EAGEEDCDGAPNPPCCDAATCKLRGACCAEGICCDQCFMKEGTICRMARGGDMDYCN 60
Db 1 EAGEEDCDGAPNPPCCDAATCKLRGACCAEGICCDQCFMKEGTICRMATDDBDDYCN 60
Cy 61 GISAGCPNPFHA 73
|||||

Db 61 GISAGCPNPFH 73

RESULT 2
US-09-832-501-37
; Sequence 37, Application US/09832501
; Publication No. US20030199043A1
; GENERAL INFORMATION:
; APPLICANT: Ballance, David J.
; APPLICANT: Sleep, Darrell
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homa
; APPLICANT: Prior, Christopher P.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS42
; CURRENT APPLICATION NUMBER: US/09/832,501
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 37
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Agkistrodon piscivorus
US-09-832-501-37

Query Match 90.6%; Score 392.5; DB 10; Length 71;

Best Local Similarity 90.3%; Pred. No. 6e-31; Indels 1; Gaps 1;

Matches 65; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 EAGEECDCGAPNPPCCDAATCKLRPGAQCAEGLCCDCCRFKKEGTICRMARGDDMDYCN 60

Db 1 EAGEECDCGSPENPCDDATCKLRPGAQCAEGLCCDCCRFKKEGTICR-ARGDDVNDYCN 59

QY 61 GISAGCPNPFH 72

Db 60 GISAGCPNPFH 71

RESULT 3
US-10-439-532-7
; Sequence 7, Application US/106439532
; Publication No. US20030186884A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
; TITLE OF INVENTION: OTHER CONDITIONS
; FILE REFERENCE: 1279-338N2/09801388
; CURRENT APPLICATION NUMBER: US/10/439,532
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US09/591,552
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 7
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Agkistrodon piscivorus
US-10-439-532-7

Query Match 90.6%; Score 392.5; DB 14; Length 71;
Best Local Similarity 90.3%; Pred. No. 6e-31; Indels 1; Gaps 1;

Matches 65; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 EAGEECDCGAPNPPCCDAATCKLRPGAQCAEGLCCDCCRFKKEGTICRMARGDDMDYCN 60

Db 1 EAGEECDCGSPENPCDDATCKLRPGAQCAEGLCCDCCRFKKEGTICR-ARGDDVNDYCN 59

QY 61 GISAGCPNPFH 72

Db 60 GISAGCPNPFH 71

RESULT 4
US-10-712-584-7
; Sequence 7, Application US/10712584
; Publication No. US20040132659A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; APPLICANT: Markland, Francis S.
; APPLICANT: Riller, Matthew
; TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAS
; TITLE OF INVENTION: OTHER CONDITIONS
; FILE REFERENCE: 1279-338N3/09801388
; CURRENT APPLICATION NUMBER: US/10/712,584
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: US09/591,552
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 08/141,321
; PRIOR FILING DATE: 1993-10-22
; PRIOR APPLICATION NUMBER: US 08/540,423
; PRIOR FILING DATE: 1995-10-10
; PRIOR APPLICATION NUMBER: US 08/632,691
; PRIOR FILING DATE: 1996-04-15
; PRIOR APPLICATION NUMBER: US 08/745,603
; PRIOR FILING DATE: 1996-11-08
; PRIOR APPLICATION NUMBER: US 09/163,047
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: US09/460,295
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 7
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Agkistrodon piscivorus
US-10-712-584-7

Query Match 90.6%; Score 392.5; DB 16; Length 71;
Best Local Similarity 90.3%; Pred. No. 6e-31; Indels 1; Gaps 1;

Matches 65; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 EAGEECDCGAPNPPCCDAATCKLRPGAQCAEGLCCDCCRFKKEGTICRMARGDDMDYCN 60

Db 1 EAGEECDCGSPENPCDDATCKLRPGAQCAEGLCCDCCRFKKEGTICR-ARGDDVNDYCN 59

QY 61 GISAGCPNPFH 72

Db 60 GISAGCPNPFH 71

RESULT 5
US-09-813-484-15
; Sequence 15, Application US/09813484
; Publication No. US20010031243A1
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: No. 6716412a1 Methods Of Ultrasound Treatment Using Gas Or Gaseou
; TITLE OF INVENTION: Filled Compositions
; FILE REFERENCE: UNGR1600
; CURRENT APPLICATION NUMBER: US/09/813,484
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 08/925,847
; PRIOR FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 15
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Completely synthetic sequence
US-09-813-484-15

Query Match 90.3%; Score 391; DB 9; Length 73;
Best Local Similarity 87.7%; Pred. No. 8.6e-31;
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGECDGAPANPCDAACTCKLRGACAGELCCDQCFMKEGTICRMARGDDMDYCN 60
DB 1 EAGEDCCGSPANPCDAACTCKLRGACGSGELCCDQCFMKEGTICRRARGDDLDYCN 60

QY 61 GISAGCPRNPLHA 73
DB 61 GISAGCPRNPLHA 73

RESULT 6
US-10-439-532-9

Sequence 9, Application US/10439532
Publication No. US2003018684A1

GENERAL INFORMATION:

APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA

TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST

TITLE OF INVENTION: OTHER CONDITIONS

FILE REFERENCE: 1279-338N2/09801388

CURRENT APPLICATION NUMBER: US/10/439,532

CURRENT FILING DATE: 2003-05-16

PRIOR APPLICATION NUMBER: US09/591,552

PRIOR FILING DATE: 2000-06-08

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn version 3.1

SEQ ID NO 9

LENGTH: 73

TYPE: PRT

ORGANISM: Trimeresurus albolabris

US-10-439-532-9

Query Match 90.3%; Score 391; DB 14; Length 73;
Best Local Similarity 87.7%; Pred. No. 8.6e-31;
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGECDGAPANPCDAACTCKLRGACAGELCCDQCFMKEGTICRMARGDDMDYCN 60
DB 1 EAGEDCCGSPANPCDAACTCKLRGACGSGELCCDQCFMKEGTICRRARGDDLDYCN 60

QY 61 GISAGCPRNPLHA 73
DB 61 GISAGCPRNPLHA 73

RESULT 7
US-10-712-584-9

Sequence 9, Application US/10712584
Publication No. US20040132659A1

GENERAL INFORMATION:

APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA

APPLICANT: Mattheuw, Francis S.

TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST

TITLE OF INVENTION: OTHER CONDITIONS

FILE REFERENCE: 1279-338N3/09801388

CURRENT APPLICATION NUMBER: US/10/712,584

CURRENT FILING DATE: 2003-11-12

PRIOR APPLICATION NUMBER: US09/591,552

PRIOR FILING DATE: 2000-06-08

PRIOR APPLICATION NUMBER: US 08/144,321

PRIOR FILING DATE: 1993-10-22

PRIOR APPLICATION NUMBER: US 08/540,423

PRIOR FILING DATE: 1995-10-10

PRIOR APPLICATION NUMBER: US 08/632,691

PRIOR FILING DATE: 1996-04-15

PRIOR APPLICATION NUMBER: US 08/745,603

PRIOR FILING DATE: 1996-11-08

PRIOR APPLICATION NUMBER: US 09/163,047
PRIOR FILING DATE: 1998-09-29

PRIOR APPLICATION NUMBER: US09/460,295

PRIOR FILING DATE: 1999-12-10

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn version 3.1

SEQ ID NO 9

LENGTH: 73

TYPE: PRT

ORGANISM: Trimeresurus albolabris

US-10-712-584-9

Query Match 90.3%; Score 391; DB 16; Length 73;
Best Local Similarity 87.7%; Pred. No. 8.6e-31;
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGECDGAPANPCDAACTCKLRGACAGELCCDQCFMKEGTICRMARGDDMDYCN 60
DB 1 EAGEDCCGSPANPCDAACTCKLRGACGSGELCCDQCFMKEGTICRRARGDDLDYCN 60

QY 61 GISAGCPRNPLHA 73
DB 61 GISAGCPRNPLHA 73

RESULT 8
US-10-046-801-15

Sequence 15, Application US/10046801
Publication No. US20030054027A1

GENERAL INFORMATION:

APPLICANT: Unger, Evan C.

TITLE OF INVENTION: Charged Lipids and Uses For The Same

FILE REFERENCE: UNG01592

CURRENT APPLICATION NUMBER: US/10/046,801

CURRENT FILING DATE: 2002-05-13

PRIOR APPLICATION NUMBER: US/09/540,448

PRIOR FILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: 08/925,353

PRIOR FILING DATE: 1997-09-08

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 15

LENGTH: 73

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: No. US20030054027A1 Sequen

US-10-046-801-15

Query Match 89.1%; Score 386; DB 14; Length 73;
Best Local Similarity 86.3%; Pred. No. 2.6e-30;
Matches 63; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAGECDGAPANPCDAACTCKLRGACAGELCCDQCFMKEGTICRMARGDDMDYCN 60
DB 1 EAGEDCCGSPANPCDAACTCKLRGACGSGELCCDQCFMKEGTICRRARGDDLDYCN 60

QY 61 GISAGCPRNPLHA 73
DB 61 GISAGCPRNPLHA 73

RESULT 9
US-10-439-532-8

Sequence 8, Application US/10439532
Publication No. US2003018684A1

GENERAL INFORMATION:

APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA

TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAS

FILE REFERENCE: 1279-338N2/09801388

CURRENT APPLICATION NUMBER: US/10/439,532

CURRENT FILING DATE: 2003-05-16

PRIOR APPLICATION NUMBER: US09/591,552
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 552
TYPE: PRF
ORGANISM: Trimeresurus gramineus
US-10-439-532-8

Query Match 89.1%; Score 386; DB 14; Length 552;
Best Local Similarity 84.9%; Pred. No. 1.5e-29;
Matches 62; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAGEBCDGCAPANPCDDATCTLRPGACAGELCCDCCRFMKEGTICRMAGDDMDYCN 60
DB 480 EAGEBCDGCSPANPCDDATCTLRPGACAGELCCDCCRFMKEGTICRMAGDDMDYCN 539

QY 61 GISACCPNPFHA 73
DB 540 GRSACCPNPFHA 552

RESULT 10
US-10-712-584-8
Sequence 8, Application US/10712584
Publication No. US20040132659A1
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
APPLICANT: Markland, Francis S.
TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST

FILE REFERENCE: 1279-338N3/09801388
CURRENT APPLICATION NUMBER: US/10/712,584
PRIOR FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: US09/591,552
PRIOR FILING DATE: 2000-06-08
PRIOR APPLICATION NUMBER: US 08/141,321
PRIOR FILING DATE: 1993-10-22
PRIOR APPLICATION NUMBER: US 08/540,423
PRIOR FILING DATE: 1995-10-10
PRIOR APPLICATION NUMBER: US 08/632,691
PRIOR FILING DATE: 1996-04-15
PRIOR APPLICATION NUMBER: US 08/745,603
PRIOR FILING DATE: 1996-11-08
PRIOR APPLICATION NUMBER: US 09/163,047
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: US09/460,295
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 552
TYPE: PRF
ORGANISM: Trimeresurus gramineus
US-10-712-584-8

Query Match 89.1%; Score 386; DB 16; Length 552;
Best Local Similarity 84.9%; Pred. No. 1.5e-29;
Matches 62; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAGEBCDGCAPANPCDDATCTLRPGACAGELCCDCCRFMKEGTICRMAGDDMDYCN 60
DB 480 EAGEBCDGCSPANPCDDATCTLRPGACAGELCCDCCRFMKEGTICRMAGDDMDYCN 539

QY 61 GISACCPNPFHA 73
DB 540 GRSACCPNPFHA 552

RESULT 11
US-10-439-532-2

Sequence 2, Application US/10439532
Publication No. US20030186884A1
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
APPLICANT: Markland, Francis S.
TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAS

FILE REFERENCE: 1279-338N2/09801388
CURRENT APPLICATION NUMBER: US/10/439,532
PRIOR FILING DATE: 2003-05-16
PRIOR APPLICATION NUMBER: US09/591,552
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 483
TYPE: PRF
ORGANISM: Agkistrodon contortrix
US-10-439-532-2

Query Match 85.0%; Score 368; DB 14; Length 483;
Best Local Similarity 83.6%; Pred. No. 7.4e-28;
Matches 61; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 EAGEBCDGCAPANPCDDATCTLRPGACAGELCCDCCRFMKEGTICRMAGDDMDYCN 60
DB 411 EAGEBCDGCAPANPCDDATCTLRPGACAGELCCDCCRFMKEGTICRMAGDDMDYCN 470

QY 61 GISACCPNPFHA 73
DB 471 GISACCPNPFHA 483

RESULT 12
US-10-712-584-2
Sequence 2, Application US/10712584
Publication No. US20040132659A1
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
APPLICANT: Markland, Francis S.
TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAS

FILE REFERENCE: 1279-338N3/09801388
CURRENT APPLICATION NUMBER: US/10/712,584
PRIOR FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: US09/591,552
PRIOR FILING DATE: 2000-06-08
PRIOR APPLICATION NUMBER: US 08/141,321
PRIOR FILING DATE: 1993-10-22
PRIOR APPLICATION NUMBER: US 08/540,423
PRIOR FILING DATE: 1995-10-10
PRIOR APPLICATION NUMBER: US 08/632,691
PRIOR FILING DATE: 1996-04-15
PRIOR APPLICATION NUMBER: US 08/745,603
PRIOR FILING DATE: 1996-11-08
PRIOR APPLICATION NUMBER: US 09/163,047
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: US09/460,295
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 483
TYPE: PRF
ORGANISM: Agkistrodon contortrix
US-10-712-584-2

Query Match 85.0%; Score 368; DB 16; Length 483;
Best Local Similarity 83.6%; Pred. No. 7.4e-28;
Matches 61; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 EAGEBCDGCAPANPCDDATCTLRPGACAGELCCDCCRFMKEGTICRMAGDDMDYCN 60
DB 411 EAGEBCDGCAPANPCDDATCTLRPGACAGELCCDCCRFMKEGTICRMAGDDMDYCN 470

QY 61 GISACCPNPFHA 73
DB 471 GISACCPNPFHA 483

RESULT 11
US-10-439-532-2

Db 411 ETGEESPDAPANPCDAATCKLTGSCAGLCCDCKFMKEGTVCRARAGDDLDYCN 470
QY 61 GISAGCPNPFHA 73
Db 471 GISAGCPNPFHA 483

RESULT 13
US-10-078-866-2
; Sequence 2, Application US/10078866
; Publication No. US20030096393A1
; GENERAL INFORMATION:
; APPLICANT: FOX, BRIAN A
; APPLICANT: SHEPPARD, PAUL O.
; TITLE OF INVENTION: Disintegrin Homolog, zsnk16
; FILE REFERENCE: 01-05
; CURRENT APPLICATION NUMBER: US/10/078,866
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/270,276
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Sistrurus miliarius
US-10-078-866-2

Query Match 83.1%; Score 360; DB 14; Length 478;
Best Local Similarity 83.6%; Pred. No. 4,4e-27;
Matches 61; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 EAGEECDCGAPANPCDAATCKLRPGAQCAEGLCCDCKFMKEGTCRMARGDDMDYCN 60
Db 406 EAGEECDCGSPENPCDAATCKLRPGAQCAEGLCCDCKFMKEGTCRMARGDDMDYCN 465
QY 61 GISAGCPNPFHA 73
Db 466 GOSADCPNPFHA 478

RESULT 14
US-10-383-588A-2
; Sequence 2, Application US/10383588A
; Publication No. US20040091887A1
; GENERAL INFORMATION:
; APPLICANT: GUO, Yaw-Wen
; APPLICANT: HO, Pei-Hsiun
; TITLE OF INVENTION: Mucroslyin and Its Gene
; FILE REFERENCE: 87146043-2001
; CURRENT APPLICATION NUMBER: US/10/383,588A
; CURRENT FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Trimeresurus mucrosquamatus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(463)
US-10-383-588A-2

Query Match 77.4%; Score 335; DB 15; Length 463;
Best Local Similarity 82.6%; Pred. No. 1.2e-24;
Matches 57; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 EAGEECDCGAPANPCDAATCKLRPGAQCAEGLCCDCKFMKEGTCRMARGDDMDYCN 60
Db 391 EAGEECDCGSPENPCDAATCKLRPGAQCAEGLCCDCKFMKEGTCRMARGDDMDYCN 450
QY 61 GISAGCPN 69

Db 451 GOSADCPN 459

RESULT 15
US-10-383-588A-8
; Sequence 8, Application US/10383588A
; Publication No. US20040091887A1
; GENERAL INFORMATION:
; APPLICANT: GUO, Yaw-Wen
; APPLICANT: HO, Pei-Hsiun
; TITLE OF INVENTION: Mucroslyin and Its Gene
; FILE REFERENCE: 87146043-2001
; CURRENT APPLICATION NUMBER: US/10/383,588A
; CURRENT FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Trimeresurus mucrosquamatus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(481)
US-10-383-588A-8

Query Match 77.4%; Score 335; DB 15; Length 481;
Best Local Similarity 82.6%; Pred. No. 1.2e-24;
Matches 57; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 EAGEECDCGAPANPCDAATCKLRPGAQCAEGLCCDCKFMKEGTCRMARGDDMDYCN 60
Db 409 EAGEECDCGSPENPCDAATCKLRPGAQCAEGLCCDCKFMKEGTCRMARGDDMDYCN 468
QY 61 GISAGCPN 69
Db 469 GOSADCPN 477

Search completed: December 3, 2004, 21:49:16
JOB time : 105 secs

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